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(54) Title: UNIVERSAL PRIMERS FOR WILDLIFE IDENTIFICATION

(57) Abstract: The invention provides novel universal primers that can amplify the fragment of cytochrome b gene of any animal species in polymerase chain reaction (PCR) and reveal the identity of the biological material of any unknown animal origin and a method for identification of the specific animal from a given biological sample.

UNIVERSAL PRIMERS FOR WILDLIFE IDENTIFICATION

TECHNICAL FIELD

The invention relates to the identification of novel universal primers that can amplify the fragment of cytochrome b gene of any animal species in polymerase chain reaction (PCR) and reveal the identity of the biological material of any unknown animal origin at species and sub-species sources. The invention also provides a method for the identification of fragments on mitochondrial cytochrome b gene in biological material of unknown origin.

BACKGROUND ART

A large number of studies in evolutionary biology utilize phylogenetic information obtained from mitochondrial cytochrome b gene. It has been identified a potent molecule to distinguish the phylogenetic depth of different lineages to family, genus and species in molecular taxonomy[1-66]. A vast database of the sequences of cytochrome b gene of different animal species has accumulated in public databases such as GenBank, NCBI (http://www.ncbi.nlm.nih.gov) etc. We have utilized this capacity of cytochrome b gene in establishing the identity of the origin of animal parts and product to its family, genus and species sources. The technique developed is based on a pair of universal primer that can amplify a small fragment of cytochrome b gene from a vast range of animal species.

Establishing identity of confiscated animal parts and products is a great challenge to law enforcement agencies because none of the methods available till date is too efficient to reveal the identity of animal remains beyond a reasonable doubt. Morphological markers, described for certain species allow the identification of complete specimen of animals[67]. However, a complete specimen is confiscated very rarely by the investigation agencies; therefore, these marker are not practical in wildlife forensics. The biochemical traits such as the bile characteristics[68] blood heam analysis[69,70] etc. have also been employed in wildlife forensic for identification of individual species. The difficulty of these markers are that these markers are limited in number and are rarely found in their natural forms in which these were originally described as the characteristic of a particular species.

The molecular approaches such as micro-satellite based identification[71], Restriction fragment length polymorphism analysis of mitochondrial genes or PCR based species specific STS markers require the prior information of the species to establish the identity[72,73]. These methods also need a significant amount of DNA material to be analysed. We may not have the prior information about the species origin of confiscated animal parts and product in forensics. therefore, these methods are not really useful and

practical in wildlife identification. The technique invented by us is universal, therefore does not require any background information to establish the identity of any unknown confiscated remains at family, genus and species sources. Being a PCR based procedure it can be applied with trace amount of any biological material. Because the amplicon length is small (472 bp); therefore, it can work perfectly with the mutilated remains, which are commonly seized by the crime investigation agencies. It does not require the large amount of genetic material i.e. DNA to be analyzed to establish the identity, hence, can detect a minute amount of adulteration in food products. The procedure described is simple and very fast. Due to the said advantages, the procedure invented by us is most suited for forensic wildlife identification.

OBJECTS OF THE INVENTION

The main object of the invention is to identify a fragment on mitochondrial cytochrome b gene capable of significantly discriminating among various evolutionary lineages of different animal species.

Another object is to identify a fragment on mitochondrial cytochrome b gene which is flanked by the highly conserved sequences at a vast range of animal species.

Yet another object is to detect a fragment on mitochondrial cytochrome b gene which is polymorphic inter-specifically, but monomorphic at intra species sources.

Still another object is to develop the universal primers to amplify the fragment on mitochondrial cytochrome b gene using polymerase chain reaction.

Another object is to develop a PCR protocol that works universally with DNA template of any unknown origin (i.e. all the animal species).

Yet another object is to provide a universal method for identification of species of analyzed material (i.e. the DNA isolated from confiscated animal remain of unknown origin) using the public databases such as GenBank, NCBI etc.

Still another object is to provide a universal method of animal identification to establish the crime with the criminal beyond a reasonably doubt.

Another object is provide a universal method to establish the identity of biological materials such as skin, horns etc confiscated from animal poachers, if it is that of an endangered species.

Yet another object is to provide a universal method for establishment of the identity of confiscated animal parts and products of endangered animal species for the purpose of production of molecular evidence of animal hunting and related crime in the court of law, so that the human violation to the wildlife resources could be controlled.

Still another object is to provide a universal technique to have an idea of the geographical location of the commitment of wildlife crime based on the haplotype of poached animal identified by the universal primer invented.

Another object is to provide a universal technique of animal identification to detect the adulteration of animal meat/products in vegetarian food product for the purpose of food fortification, by the food fortification agencies.

Yet another object is to provide a universal technique for detection of the origin of blood or blood stains etc collected from the scene of crime related to offences such as murder, rape etc, in order to establish the origin of blood found at scene of crime when it sounds as if criminals have wontedly spread the blood of an animal at the scene of crime, to confuse the crime investigation agencies and forensic scientists with human blood.

Another object is to invent and authenticate a universal technique that can be converted to a (a) 'MOLECUALR KIT' and (b) 'DNA CHIPS' based application to meet the requirements of above objectives.

SUMMARY OF THE INVENTION

Accordingly, the invention provides novel universal primers that can amplify the fragment of cytochrome b gene of any animal species in polymerase chain reaction (PCR) and reveal the identity of the biological material of any unknown animal origin

DETAILED DESCRIPTION OF THE INVENTION

Keeping in view the above objectives, the cytochrome b gene sequences (1140 bp) of 221 distantly related animal species (listed in Table 1) representing various families were obtained from public database NCBI (http://www.ncbi.nlm.nih.gov). These sequences were aligned using the software *Clustal X(1.8)*(NCBI, USA) and a fragment (of 472 bp, alignment shown in Table 2) of gene was identified which had all the features mentioned above under column 1, 2 and 3 of sub-heading 'Objectives of invention'. As for the identity of this fragment we would like to mention that it includes the nucleotides between 398 to 869 in *Antilope cervicapra* and *Felis catus*; however, 399 to 870 in *Homo sapiens sapiens* species. Except at few positions (marked as star (*) in Table 2, the nucleotide sequences of this fragment are highly variable amongst the animal species, giving rise to their unique molecular signature. These molecular signatures are characteristic of its species and form the basis of revealing the identity of the biological material of an unknown animal origin by the procedure invented by us. Considering *Antilope cervicapra* as a representative species, the sequence of this fragment is mentioned herewith:

Mitochondrial cytochrome b gene sequence (398-869 bp) of *Antilope cervicapra*:

"taccatgaggacaaatatctttttgaggagcaacagtcatcaccaatctcctttcagcaatcccatacatcggtacaaacctagtaga atgaatctgaggagggttctcagtagataaagcaacccttacccgatttttcgccttccactttatcctcccatttatcattgcagcctt accatagtacacctactgtttctccacgaaacaggatccaacaaccccacaggaatctcatcagacgcagacaaaattccattccac ccctactacactatcaaagatatcctaggagctctactattaattttaaccctcatgcttctagtcctattctcaccggacctgcttggag acccagacaactatacaccagcaaacccacttaatacacccccacatatcaagcccgaatgatacttcctatttgcatacgcaatcct ccgatcaattcctaacaaactaggagg".

A pair of universal primer was designed to amplify this fragment in polymerase chain reaction (PCR). These primers were named as 'mcb398' and 'mcb869' because of its property to amplify a region of mitochondrial cytochrome b gene between nucleotides 398 to 869 of *Antilope cervicapra,* a representative animal species for this invention. We took this animal species as representative species because the idea of developing such a novel primers came in the mind of inventors while they were working on the genome of this animal in Centre for Cellular and Molecular Biology, Hyderabad, India. These primers work universally because its 3' end are highly conserved amongst a vast range of animal species (shown in Table 2). As mentioned above, the DNA fragment (sequence of which is shown above) targeted by these primers is highly polymorphic inter-specifically; however, it is monomorphic among the individual of same species (Tables 6, 7a, 7b, 7c, 7d and 8, respectively). These unique features of the targeted region enable these primers to generate the molecular signatures of an individual species; thereby, enabling them to differentiate amongst the animals of different species (see in Figure 1c). The variation within the fragment amplified by these primers increase with increasing distances of evolutionary lineages of two animals (Table 8). These unique features of the fragment amplified by the universal primers 'mcb398' and 'mcb869' invented by the applicants fulfill the objectives of invention.

Thus, the primers invented by us can generate the molecular signature from any biological material of unknown animal origin, which actually is the characteristic of its family, genus and more precisely, the species. When these signatures are compared *in-silico* with the signatures already available in public databases (viz., GenBank, NCBI database etc) using '*BLAST* software[73], it indicates identity of the family, genus or species of the analyzed material, which in turn is confirmed practically by comparing with the reference animals of the revealed family, genus or species, by including them in the further analysis by the primers 'mcb398' and 'mcb869'. The complete procedure involved in the *analyses* (the word, *'analyses'* should be understood with the stepwise procedure to establish the identity of the biological remain of any unknown animal origin for the aims mentioned in columns

1-13 under sub-heading 'Objectives of invention') is briefed under 'Examples 5 and 6, respectively, as well as illustrated in Figures 1a, 1b and 1c, respectively.

BRIEF DESCRIPTION OF DRAWING AND TABLES

Figure 1a. Illustration of the step-wise procedure involved in *analyses*. The unknown biological material i.e. 'adil.flesh' refers to the confiscated skin mentioned in 'Example 6'. The arrow marks indicate the stepwise procedure involved. The brief description of Figure 1a is as follows:

The biological material i.e. the confiscated skin 'adil.flesh' was subjected to DNA isolation using the standard procedures[74]. The DNA obtained was amplified using the primers 'mcb398' and 'mcb869' in PCR, fractionated in 2% (w/v) agarose gel, visualized and photographed under UV light using Gel Documentation System (Syngene, USA). The lane 'M' shown in the photograph represents the molecular weight marker (Marker XIII, Boehringer mannheim). Lane 1 shows the PCR amplicon (472 bp) obtained from 'adil.flesh' using primers 'mcb398' and 'mcb869'. The PCR amplicon obtained were sequenced at both the strand using "ABI Prism 3700 DNA Analyzes, PE-Applied Bio-systems). The chromatogram shows the sequences (about 80 bp long, i.e. between 150-230 bp of sequence (328 bp), revealed from the PCR product of 472 bp length) obtained from 'adil.flesh'.

Figure 1b. Illustrates the further steps involved in *analyses*. The sequence (328 bp) revealed from 'adil.flesh' was subjected to homology search in *nr (i.e. non-redundant)* database of Netional Centre for Biological Information (NCBI), USA. The sequences producing significant alignments are shown along with its bits score and E values. It indicates the extent of homology amongst the sequence enquired (i.e. the 328 bp sequence from adil.flesh) and the sequences registered in *nr* database of NCBI. BLAST analysis revealed the highest homology of the sequence revealed from 'adil.flesh' with the sequence of *Panthera pardus* (gene bank registration number 'AY005809'), indicating the identity of adil.flesh as that of a leopard (*Panthera pardus*) origin. Figure 1b further illustrates the multiple alignments of the sequences obtained from reference animals (listed in Table 5) along with the sequence obtained from 'adil.flesh'. The sequences of 'adil.flesh' is similar to the sequences of 'gz1L' further confirming the identity of the source of confiscated remain 'adil.flesh' as that of a *Panthera pardus* origin.

Figure 1c illustrates the NJ-tree (Neighbor Joining tree) constructed using CLUSTAL X (1.8) from the sequences revealed from 'adil.flesh' and reference animals listed in Table 5.

The animals belonging to similar species cluster together; however, the animals of different species group in different clusters. The confiscated material under investigation (i.e. 'adil.flesh') clusters with 'gz1L' (i.e. the known normal leopard *'Panthera pardus'*) indicating the identity of the species of 'adil.flesh' as that of a *Panthera pardus* source.

Figure 2 shows the Agarose gel electrophorogram showing the PCR amplicons (472 bp) obtained from the reference animals of family felidae listed in Table 5, using universal primers 'mcb398 and 'mcb869'. Description of different lanes is as follows:

Lanes 1-21: The PCR profiles of the animals 1-21, respectively, listed in Table 5.

Lane 22: The PCR profiles of DNA isolated from confiscated skin of unknown animal origin 'i.e. adil.flesh'

Lane 23: Negative control (no DNA)

Lane M: Molecular weight marker (marker XIII, Boehringer mannheim)

Figure 3. Shows PCR amplicons obtained from animals listed in Table 9. The primers used in PCR are 'AFF' and 'AFR'. The description of different lanes shown is as follows:

Lane 1-4: The PCR profiles of animals 1-4, respectively, listed in Table 9, showing amplicons of 354 bp.

Lane M: Molecular weight marker (marker XIII, Boehringer mannheim)

Figure 4. Shows PCR amplicons obtained from animals listed in Table 12. This experiment demonstrates the universal nature of our primers among a vast range of animal species. Description of different lanes shown is as follows:

Lanes 1-23: The PCR profiles of the animals 1-23, respectively, listed in Table 12. The PCR product of 472 bp is amplified universally from all the animal species analyzed.

Lane 24: Negative control (no DNA)

Lane M: Molecular weight marker (marker XIII, Boehringer mannheim)

Table 1. List of 221 animal species used for *In-silico* analysis to design the universal primers *'mcb398' and 'mcb869'. Table also demonstrate the* 'P,S *scores'* of 'mcb398' and 'mcb869' for different templates. The descriptions of various symbols used in this table are as follows:

Symbol (#) refers to Number

Symbol (*) refers to the animal species which is either protected species (listed in Wildlife (Protection) Act , 1972 (Central Act NO 53 of 1972), or an endangered/rare animal species

Symbol (^{S}P,S/F) refers to Probability of match and Stability of match of primer 'mcb398' with different templates (i.e. the cytochrome b gene from different species origin). A higher P, S score refers to the higher probabilities of significant amplification of specific

template by the primer. It is calculated by *Amplify (1.2)* software.

Symbol ($^{\Psi}$P,S/R) refers to Probability of match and Stability of match of primer 'mcb869' with different templates. A higher P,S score refers to the higher probabilities of significant amplification of specific template by the primer. It is calculated by *Amplify (1.2)* software.

Table 2. Multiple sequence alignment of 472 bp fragment of mitochondrial cytochrome b gene (identified by inventors to fulfill the requirements of column 1, 2 and 3 mention under sub-heading 'Objectives of invention') of 221 animal species listed in Table 1. Alignments also show the binding sites for universal primers 'mcb398' and 'mcb869'. The symbol (*) refers to the nucleotide bases which are conserved amongst 221 animal species listed in Table 1). The alignments have been done using software *CLUSTAL X (1.8)*. The nucleitide positions that are unmarked are variable amongst 221 animal species analyzed. These variable sites together constitute the molecular signature of an individual species, giving rise to molecular basis of species identification by our primers.

Table 3. Results of the blast analysis of the sequence revealed from 'adil.flesh' in '*mito*' database of NCBI. It shows the most significant alignment of cytochrome b sequence (328 bp) revealed from confiscated skin piece 'adil.flesh' with *felis catus* cytochrome b gene sequence (genbank registration number NC_001700.1, bits score 365, E value, e-101) registered in NCBI database (bits score 365 and E value e-101). It gives an indication that the species of analyzed material belongs to family felidae. It also fulfills the requirements of column 6 mention above under sub-heading 'Objectives of invention'.

Table 4. Results of the blast analysis of the sequence revealed from 'adil.flesh' in '*nr*' database of NCBI. It shows the most significant alignment of cytochrome b sequence (328 bp) revealed from confiscated skin piece 'adil.flesh' with *Panthera pardus* cytochrome b gene sequence (genbank registration number AY005809, bits score 603, E value, e-170) registered in NCBI database. It gives an indication that the species of analyzed material belongs to *Panthera paurdus* origin. It also fulfills the requirements of column 6 mention above under sub-heading 'Objectives of invention'.

Table 5. Reference animal belonging to family felidae selected for comparison with 'adil.flesh' to confirm the findings of BLAST analysis results of which are mentioned in Table 3 and 4, respectively. The animals listed in SN. 1-21 represent different species of family felidae. SN. 22 and 23 are primate species taken for out-group comparisons.

Table 6 Multiple sequence alignments of cytochrome b sequences (328 bp) revealed from 'adil.flesh' and reference animals listed in Table 5. The positions that have a common nucleotide in all the animal species under investigation are shown with a star (*) mark;

however, the positions that are variable in any of the animals under investigation are unmarked. The nucleotides at these positions constitute the molecular signature of an individual species, which are unique and highly specific for its species. These signatures are the molecular basis of identification of individual animal species using our primers 'mcb398' and 'mcb869'.

Table 7 (Tables 7a, 7b, 7c and 7d). The comparison of the molecular signatures of different animal species investigated along with 'adil.flesh', the confiscated skin of unknown animal origin. This table demonstrates the variable positions (i.e. the positions which are not marked with star (*) symbol in Table 6), amongst the 328 bp fragment revealed from the animals listed in Table 5. The dot (.) mark represents the presence of the similar nucleotide as listed in lane 1 i.e. the sequence from "adil.flesh' at that position. It demonstrates that the signatures of each species are unique and specific to its species. The molecular signatures of 'adil.flesh' are comparable (except for position 37 which has a transition from 'T' to 'C') to the molecular signature of 'gz1L' i.e. the known leopard *'Panthera pardus'* source, indicating the identity of the source of confiscated skin 'adil.flesh' as that of a leopard *'Panthera pardus'* source. The nucleotide variations (at the positions 153, 198, 223, 264, among the known leopards, (i.e. gz1L, gz2L, and gz3L, respectively)), give an idea about the geographical habitat of each animals. Various studies referring to molecular evolution of different animal species support this hypothesis[75]; however, it could further be confirmed by taking the reference animals from different geographical areas and analyzing by our primers 'mcb 398' and 'mcb869'. If we could generate the database of different haplotypes (i.e. habitat specific molecular signatures) of the animal species, it would also enable our primers to reveal the geographical location of the commitment of wildlife crime.

Table 8. Percent similarity matrix calculated by pair-vise comparisons of nucleotide sequences aligned (illustrated in Table 6). The cytochrome b gene sequence of DNA isolated from confiscated material had maximum similarity (99.7% and 98.2%, with the lineages of animals 'gz2L' and 'gz3L', respectively) with the sequences obtained from known normal leopard source, indicating its identity as that of a leopard origin. The similarity matrix has been calculated using the software *PHYLIP (3.5)*.

Table 9. Animals selected for validation of minimum P,S score for efficient amplification of cytochrome b gene of different origin by the primers 'mcb398' and 'mcb869'. P,S score of primers 'AFF' and 'AFR' for these animals are shown.

Table 10. BLAST analysis of primers 'mcb398' in *nr* database of NCBI . It demonstrates

that the 3' end of this primer is highly conserved among a vast range of animal species. It also shows the significant homology among the primer and templates (i.e. the cytochrome b gene fragment of different animal species), confirming the universal nature of our primer

Table 11. BLAST analysis of primers 'mcb869' in *nr* database of NCBI. It demonstrates that the 3' end of this primer is highly conserved among a vast range of animal species. It also shows the significant homology among the primer and templates (i.e. the cytochrome b gene fragment of different animal species), confirming the universal nature of our primer.

Table 12. Other animal belonging to distantly related animal species, investigated to confirm the universal nature of primers 'mcb398' and 'mcb869'. Gel photograph showing the PCR amplicons from these animals are shown in Figure 4.

The mitochondrial cytochrome b gene has very widely been used in molecular taxonomic studies. It has immense capabilities to reveal different evolutionary lineages of animals in family, genus and species specific manner. It has also been used to classify the population of a particular species according to its demographic distributions[75]. The vast database of cytochrome b sequences of different animal species has accumulated in public databases such as Genbank and NCBI[1-65]. We have explored these unique characteristics of cytochrome b gene to establish the identity of confiscated remains of any unknown animal by inventing a pair of novel primers, 'mcb398' and 'mcb869', that can amplify a small fragment (472 bp) of cytochrome b gene of wide range of animal species in universal manner. These primers work universally because its 3' ends target within a highly conserved region.

The fragment of cytochrome b gene identified had all the features mentioned in columns 1, 2 and 3 listed under sub-heading 'Objective of invention'. We identified this fragment by aligning the cytochrome b gene sequences (1140 bp) of 221 different animal species listed in *Table 1. These sequences are publicly available in NCBI DNA databases. These* sequences were aligned using the software *CLUSTAL X (1.8).* As mentioned before, the 472 bp fragment of cytochrome b gene identified by us to have the features mentioned in columns 1, 2 and 3 listed under sub-heading 'Objective of invention' includes the nucleotides between 398 to 869 in *Antilope cervicapra* and *Felis catus*; however, 399 to 870 in *Homo sapiens sapiens* species. Except at few positions (marked as star (*) in Table 2, the nucleotide sequences of this fragment are highly variable amongst the animal species, revealing the identity of the biological material belonging to that of an unknown animal origin by the procedure invented by us. As for identity of this fragment we are

considering *Antilope cervicapra* as a representative species, and the sequence the above fragment of cytochrome b gene of *Antilope cervicapra* is mentioned herewith:

Mitochondrial cytochrome b gene sequence (398-869 bp) of *Antilope cervicapra*

"taccatgaggacaaatatcttttgaggagcaacagtcatcaccaatctcctttcagcaatcccatacatcggtacaaacctagtaga
atgaatctgaggagggttctcagtagataaagcaacccttacccgatttttcgccttccactttatcctcccatttatcattgcagcccct
accatagtacacctactgtttctccacgaaacaggatccaacaaccccacaggaatctcatcagacgcagacaaaatccatttccac
ccctactacactatcaaagatatcctaggagctctactattaattttaaccctcatgcttctagtcctattctcaccggacctgcttggag
acccagacaactatacaccagcaaacccacttaatacacccccacatatcaagcccgaatgatacttcctatttgcatacgcaatcct
ccgatcaattcctaacaaactaggagg

Table 2 presents the alignment of the above fragment of cytochrome b gene of 221 animal species. Each species in table 2 has been represented by a unique code, which is decoded in Table 1. We selected these species to represent the vast range of animal families of distant orders. Of 221 species, about 65 were the protected/endangered or rare species listed in Wildlife (Protection) Act , 1972 (Central Act NO 53 of 1972). These species are marked with symbol (*) in Table 1. The NCBI accession number refers to its registration number in NCBI database and the number in superscript represent the reference cited. Based on the aligned cytochrome b sequences of different 221 animal species the primers designed were as follow:

Primers name	Sequence (5'-3')
'mcb398'	"TACCATGAGGACAAATATCATTCTG"
'mcb869'	"CCTCCTAGTTTGTTAGGGATTGATCG"

Tables 2, 10 and 11, respectively, demonstrates that the 3' ends of the primers are highly conserved amongst all the animal species analyzed *in-silico* (In total 221 animal species listed in Table 1 and about 500 species listed in Tables 10 and 11, respectively) Also, the 5' end of the primers were selected within the conserved region of cytochrome b gene to *improve the probability and stability of match of the primers to their target sequences* (i.e. the above mentioned 472 bp fragment of cytochrome b gene). The primers were thoroughly checked for internal stabilities, loop or dimmer formation using different software viz., 'Amplify (1.2)', 'Primer3' (http://www.genome.wi.mit.edu/cgi-bin/primer/primer3.cgi) as well as manually. . We assigned the P,S score (P=Probability of match, S=Stability of match) to the primers for each template using the software *Amplify (1.2)*. The higher scores of P and S ensure a good amplification if all other conditions standard (which are mentioned under 'Example 3') are optimum. The Highest score for 'mcb398' was 98.63 (i.e. the situation where the primer has perfect match with template);

however, the highest P, S for 'mcb869' was recorded as 98, 68 for a complete match between the primer and template. The lowest P,S score observed for 'mcb398' was 81,50 for species *Talpa europaea* whereas 'mcb869' had a high P, S score for this species (92, 57). The another species which have lowest P, S score for one of the two primers were *Eumeces egregious* and *Equus ainus*. *Eumeces egregious* had P, S score 86, 55 and 73,51 for 'mcb398' and 'mcb869', respectively; however, the P, S score of *Equus ainus was calculated as* 91,61 and 73, 51 for 'mcb398' and 'mcb869', respectively. All other animals had higher P, S scores then the above mentioned species. To ensure that these primers would work efficiently with the DNA template from the animals having the lowest P, S score for one of the primers, we designed an another experiment to validate the lower limits of one of the two primers sufficient for efficient amplification in PCR. We designed an another primer pair (AFF= 5'tagtagaatgaatctgaggagg3' and AFR=5'atgcaaataggaagtatcattc3'.) having more mis-pairing at their annealing sites (but not at ends), therefore have less internal stability and lower P, S scores for its templates (listed in Table 9). The P,S scores of 'AFF' and 'AFR' were as calculated as low as 41 and 49 for *Platanista gangetica* and *Sus scrofa* These species were amplified efficiently using the primers 'AFF' and 'AFR' (results shown in Figure 3) (keeping all other conditions standard i.e. the conditions mentioned in 'Example 3'). The lowest P,S scores (86, 55 and 73,51 for species *Eumeces egregious*) for our primers 'mcb398' and 'mcb869', respectively, were higher then the above range of combined P, S scores of 'AFF' and 'AFR' for species *Sus scrofa* (87, 52 and 87, 41), which was efficiently amplified by the primers 'AFF' and 'AFR'. It gives an indication that the primers 'mcb 398' and 'mcb 869' would work with all the species including *Eumeces egregious* efficiently to give rise to the expected product in PCR. This experiment confirmed that the primers 'mcb398' and 'mcb 869' are capable of amplifying the cytochrome b fragment of most of the animal species in a universal manner.

For further confirmation of universal nature of our primers, we blasted the sequence of our primers against the *mito* and *nr* databases of NCBI using BLAST software. The results of these analyses are shown in Tables 10, and 11, respectively.

Finally, the universal nature of the primers was tested in our laboratory with some more animal species listed in Table 12. These primers amplified all the animal species efficiently, giving rise to the band of expected size (472 bp). The results are shown in Figure 4. This experiments substantiated the results of P,S analysis and other *in-silico* analyses to show that the primers 'mcb398'and 'mcb 869' are universal primers.

The flow chart of establishing identity of the species of biological material of unknown animal origin using primers 'mcb398' and 'mcb869'

Biological material of unknown animal origin

↓

DNA isolation

↓

PCR amplification of DNA isolated using primers 'mcb398' and 'mcb869'

↓

Sequencing at both the strands in triplicate (using any standard procedure of sequencing such as using ABI Prism 3700, PE-Applied Bio-systems)

↓

BLAST of revealed sequence in *mito* database of NCBI (http://www.ncbi.nlm.nih.gov/BLAST (it gives idea about the family of the analyzed material by producing the most significant alignment of the query sequence with the sequences registered in database)

↓

BLAST of revealed sequence in *nr* database of NCBI (http://www.ncbi.nlm.nih.gov/BLAST (it gives idea about the Genus or more precisely, species of the analyzed material by producing the most significant alignment of the query sequence with the sequences registered in database)

↓

Selection of reference animals belonging to the family/Genus/and species revealed by *mito* and *nr* BLAST searches

↓

Isolation of DNA from the blood of known reference animals; PCR amplification using primers 'mcb398' and 'mcb869' ; sequencing of the PCR products in triplicate using the same primers

↓

Multiple sequence alignments of the revealed sequences of mitochondrial cytochrome b gene of known reference animals and the biological material of unknown animal origin using software such as *Autoassembler (/CLUSTAL X (1.8)*

↓

Identification of sequence from the aligned sequences that is homologous (or significantly similar) to the cytochrome b gene sequence of the DNA obtained from biological material of unknown animal origin.

↓

The species of homologous sequence would be the species of the biological material under investigation

Examples

Example 1

Example for identification of a fragment of cytochrome b gene fulfilling the requirements of columns 1, 2 and 3 mentioned under sub-heading 'Objectives of invention' of heading 'Brief summary of invention'

The cytochrome b molecule has very vastly been used in molecular taxonomic studies. Being a slow evolving gene, It has a tremendous information in its nucleotide sequences to distinguish the animals to their family, genus and species sources[1-65]. A vast database of the sequences of cytochrome b gene of different animal species has accumulated in the *nr* and *mito* databases of NCBI. We have explored these qualities of cytochrome b gene to establish the identity of confiscated remains of unknown animal origin to its family, genus and species sources. For this purpose, we have identified a fragment of cytochrome b gene which is highly polymorphic inter-specifically, however, it is monomorphic among the individual of same species, therefore it can group the individual of an unknown species with the known individuals of reference species to which it belongs. In order to amplify this fragment from DNA isolated form any unknown origin, it was necessary that it remain flanked with the highly conserved sequences amongst a vast range of animal families. To identify such a unique fragment within the cytochrome b gene, we aligned the sequences of 221 distantly related animal species (listed in Table 1) representing various families using software CLUSTAL X (1.8). These sequences were obtained from public database NCBI (http://www.ncbi.nlm.nih.gov). The aligned data was examined carefully for the conserved sites amongst all the species included in *in-silico* analysis. We identified a fragment (472 bp) of cytochrome b gene that was fulfilling all the requirements mentioned above and also under column 1, 2 and 3 of sub-heading 'Objectives of invention'.

As for the identity of this fragment we would like to mention that it includes the nucleotides between 398 to 869 in *Antilope cervicapra* and *Felis catus*; however, 399 to 870 in *Homo sapiens sapiens* species. Except at few positions marked as star (*) in Table 2, the nucleotide sequences of this fragment are highly variable amongst the animal species, giving rise to their unique molecular signature. These molecular signatures are characteristic of its species and form the basis of revealing the identity of the biological material of an unknown animal origin by the procedure invented by us. Considering *Antilope cervicapra* as a representative species, the sequence of this fragment is mentioned herewith:

Mitochondrial cytochrome b gene sequence (398-869 bp) of *Antilope cervicapra*

"taccatgaggacaaatatctttttgaggagcaacagtcatcaccaatctcctttcagcaatcccatacatcggtacaaacctagtaga
atgaatctgaggagggttctcagtagataaagcaacccttacccgatttttcgccttccactttatcctcccatttatcattgcagcccct
accatagtacacctactgtttctccacgaaacaggatccaacaaccccacaggaatctcatcagacgcagacaaaattccattccac
ccctactacactatcaaagatatcctaggagctctactattaattttaaccctcatgcttctagtcctattctcaccggacctgcttggag
acccagacaactatacaccagcaaacccacttaatacacccccacatatcaagcccgaatgatacttcctatttgcatacgcaatcct
ccgatcaattcctaacaaactaggagg"

Example 2:

Example for development of universal primers to amplify the fragment identified mentioned under 'Example 1'.

A pair of universal primer was designed which has the following features:

1. It targets the fragment identified (mentioned under 'Example 1') to amplify it in polymerase chain reaction (PCR).
2. Its 3' and 5' ends that are highly conserved (marked as star (*) in Table 2), amongst a vast range of animal species ensuring the amplification of the fragment mentioned above in a universal manner. The sequencing of the fragment amplified by these primes reveals the molecular signature of the species of analyzed material, which on comparison with the sequences of the known reference animals reveals the identity of the species of unknown biological material under investigation.
3. The tm (melting temperature) of both primers was almost similar (about 58 degree centigrade) ensuring the significant annealing of both the primers to its template, therefore significant amplification of targeted region in PCR.
4. The internal stability and P, S, score of the primers were ensured higher while designing it. The possibilities of internal loop formation, dimmer formation etc were also excluded by selecting its sequence uniquely. This ensured that the primer would be a good primer to be used in PCR for amplification of DNA from unknown animal origin.
5. The 3' end of the primers were ensured to have either 'G' or 'C' to increase the probability of strong bonding at its 3'ends, which is necessary for efficient amplification of DNA template in PCR. It also strengthens the universal nature of the primer.
6. The sequences of the primers were ensured to be unique so that it does not give rise to non-specific and spurious products in PCR leading to confusion. It improved the efficiency and quality of the technique invented by us.

7. These primers were named as 'mcb398' and 'mcb869' because of its property to amplify a region of mitochondrial cytochrome b gene between nucleotides 398 to 869 of *Antilope cervicapra,* a representative animal species for this invention. We took this animal species as representative species because the idea of developing such a novel primers came in the mind of inventors while they were working on the genome of this animal in Centre for Cellular and Molecular Biology, Hyderabad, India.
8. The sequences of the universal primers invented are as follows:

Primers name	Sequence (5'-3')
'mcb398'	"TACCATGAGGACAAATATCATTCTG"
'mcb869'	"CCTCCTAGTTTGTTAGGGATTGATCG"

Example 3:

Example for development of universal PCR conditions to ensure the amplification of a template of any unknown origin in PCR, hence strengthening the universal nature of the technique invented by us

The PCR conditions developed had the following unique features:

1 These were capable of amplifying the DNA template of any animal origin in an universal manner using the universal primers mentioned under 'Example 2'.

2. The conditions were selected to ensure the comparable annealing temperature for both the primers i.e. 'mcb398' and 'mcb869'.

3. The PCR conditions standardized herewith are universal; therefore, the possibility of PCR failure with a template of unknown origin due to non-standard conditions is excluded. It ensures the universal nature of our technique to be used in wildlife forensics.

4. *The universal conditions mentioned above are:*

Amplification reactions should be carried out in 20 µl reaction volume containing approximately 20 ηg of template DNA, 100µm each of dNTPs, 1.25 pmole of each primer, 1.5mM $MgCl_2$, 0.5 unit of Ampli*Taq* Gold (Perkin-Elmer-Cetus, USA) DNA polymerase and 1X PCR buffer (10mM Tris-HCl, pH 8.3, and 50mM KCl). The amplification profiles followed should be: an initial denaturation at 95^0C for 10 min, followed by 35 cycles each of denaturation at 95^0C for 45 s, annealing at 51^0C for 1 min, and extension at 72^0C for 2 min. The extension step at 35^{th} cycles should be held for 10 min.

Example 4:

Establishing the universal nature of our primer and experimental evidences to demonstrate the universal nature of primers:

The universal nature of the primers 'mcb398' and 'mcb 869' was ensured by the following measures:

(a) Selecting the primers from the aligned cytochrome b gene sequences of 221 animal of distantly related species:

The cytochrome b gene sequences (1140 bp) were aligned using software *CLUSTAL X (1.8)*. The region of cytochrome b gene that was most conserved amongst 221 animal species was selected to design the primers.

(b) Selecting the 3' and 5' ends of the primers at the highly conserved positions of cytochrome b gene:

The 3' and 5' ends of the primers were ensured to anneal to a highly conserved position amongst 221 animal species representing a vast range of animal families. It was done to ensure an efficient amplification of all the species in PCR. These positions are shown with star (*) mark in Table 2.

(c) Ensuring either 'G' or 'C' at the 3' end of the primers:

It was ensured the primers to have either 'G' or 'C' at its 3' ends as these are the nucleotides that ensure the strong bonding at the 3' ends of the primers due to three hydrogen bonds while pairing with each other. The strong bonding at 3' ends helps the primers to anneal properly with its template resulting in significant amplification in PCR.

(d) Selecting the sequences of the primers to ensure a higher internal stability, higher P, S score, and no primer dimmer and loop formation:

The sequences of the primers were selected to have a high P, S score for a vast range of animal species (Shown in Table 1). The care was taken to exclude the possibilities of loop *or primer dimmer formation that could reduce the efficiency of the primers* in PCR.

(e) Selecting the sequence of the primers with a comparable melting temperature:

The sequences of the primers were selected to have a comparable melting temperature so that these could work together to amplify a DNA template in PCR at a similar annealing temperature. The melting temperature of both the primers was about 58 degree centigrade and the annealing temperature used in PCR is 51 degree centigrade.

Experimental evidences to demonstrate the universal nature of primers:

(1) Evidence from *In-silico* analysis :

(a) Selecting the primers within the most conserved region of mitochondrial cytochrome b gene

As mentioned above, the primers were designed to anneal within a highly conserved region of mitochondrial cytochrome b gene fragment of 472 bp. Table 2 presents the alignment of the above fragment of cytochrome b gene of 221 animal species representing a vast range of animal families. The conserved positions of nucleotide sequences are shown with star (*) mark in Table 2

Table 2 also demonstrates that the 3' ends of the primers are highly conserved amongst all the animal species analyzed *in-silico.* In the aligned sequences, the conserved nucleotides are marked with symbol (*). Also, the 5' end of the primers were selected within the conserved region of cytochrome b gene to improve the probability and stability of match of the primers to their target sequences (i.e. the above mentioned 472 bp fragment of cytochrome b gene). The primers were thoroughly checked for internal stabilities, loop or dimmer formation using different software viz., *'Amplify (1.2)', 'Primer3'* (http://www.genome.wi.mit.edu/cgi-bin/primer/primer3.cgi) as well as manually.

(b) P, S, score analysis:

We assigned the P,S score (P=Probability of match, S=Stability of match) to the primers for each template using the software *Amplify (1.2).* The higher scores of P and S ensure a good amplification if all other conditions standard (which are mentioned under 'Example 3') are optimum. The Highest score for 'mcb398' was 98,63 (i.e. the situation where the primer has perfect match with template); however, the highest P, S for 'mcb869' was recorded as 98, 68 for a complete match between the primer and template. The lowest P,S score observed for 'mcb398' was 81,50 for species *Talpa europaea* whereas 'mcb869' had a high P, S score for this species (92, 57). The another species which have lowest P, S score for one of the two primers were *Eumeces egregious* and *Equus ainus. Eumeces egregious* had P, S *score 86, 55 and* 73,51 for 'mcb398' and 'mcb869', respectively; however, the P, S score of *Equus ainus was calculated as* 91,61 and 73, 51 for 'mcb398' and 'mcb869', respectively. All other animals had higher P, S scores then the above mentioned species. To ensure that these primers would work efficiently with the DNA template from the animals having the lowest P, S score for one of the primers, we designed an another experiment to validate the lower limits of one of the two primers sufficient for efficient amplification in PCR. We designed an another primer pair (AFF= $^{5'}$ctagtagaatgaatctgaggagg$^{3'}$ and AFR= $^{5'}$tatgcaaataggaagtatcattc$^{3'}$.) that have more mis-pairing at their annealing sites (but not at ends), therefore have less internal stability

and lower P, S scores for its templates (listed in Table 9). The P,S scores of 'AFF' and 'AFR' were as calculated as low as 41 and 49 for *Platanista gangetica* and *Sus scrofa* These species were amplified efficiently using the primers 'AFF' and 'AFR' (results shown in Figure 3) (keeping all other conditions standard i.e. the conditions mentioned in 'Example 3'). The lowest P,S scores (86, 55 and 73,51 for species *Eumeces egregious*) for our primers 'mcb398' and 'mcb869', respectively, were higher then the above range of combined P, S scores of 'AFF' and 'AFR' for species *Sus scrofa* (87, 52 and 87, 41), which was efficiently amplified by the primers 'AFF' and 'AFR'. It gives an indication that the primers 'mcb 398' and 'mcb 869' would work with all the species including *Eumeces egregious* efficiently to give rise to the expected product in PCR. This experiment confirmed that the primers 'mcb398' and 'mcb 869' are capable of amplifying the cytochrome b fragment of most of the animal species in a universal manner.

© BLAST analysis:

The sequences of primers 'mcb398' and 'mcb869' were blasted against mito and nr databases of NCBI to see its significant alignments with the sequences registered in GenBank. As expected, the most significant alignments of the sequences were found with the cytochrome b gene regions (within the 472 bp fragment mentioned in 'Example 1') of different animal species. This analysis also showed that the 3' as well as 5' ends of the primers were highly conserved amongst a vast range of animal species, confirming the universal nature of the primers (Tables 10 and 11, respectively)

(2) Evidence from bench work/experiments done in laboratory conditions:

The DNA from different animals belonging to distantly related species (mentioned in Table 12) was isolated and subjected to PCR amplification using the primers invented by us i.e. the primers 'mcb398' and 'mcb869' The PCR products amplified were resolved in agarose gel by electrophoresis and visualized under UV light. The PCR products of expected size (472bp) were obtained from all the animals confirming the universal nature of our primers. These results are shown in Figure 4.

Example 5:

Example to establish the identity of confiscated remains from unknown animal origin using the universal primers 'mcb398' and 'mcb869'.

The step-vise procedure to establish the identity of the biological material from an unknown animal source is mentioned below:

Biological material of unknown animal origin

DNA isolation

↓

PCR amplification of DNA isolated using primers 'mcb398' and 'mcb869'

↓

Sequencing at both the strands in triplicate (using any standard procedure of sequencing such as using ABI Prism 3700, PE-Applied Bio-systems)

↓

BLAST of revealed sequence in *mito* database of NCBI

(http://www.ncbi.nlm.nih.gov/BLAST

(it gives idea about the family of the analyzed material by producing the most significant alignment of the query sequence with the sequences registered in database)

↓

BLAST of revealed sequence in *nr* database of NCBI

(http://www.ncbi.nlm.nih.gov/BLAST

(it gives idea about the Genus or more precisely, species of the analyzed material by producing the most significant alignment of the query sequence with the sequences registered in database)

↓

Selection of reference animals belonging to the family/Genus/and species revealed by *mito* and *nr* BLAST searches

↓

Isolation of DNA from the blood of known reference animals;
PCR amplification using primers 'mcb398' and 'mcb869' ; sequencing of the PCR products in triplicate using the same primers

↓

Multiple sequence alignments of the revealed sequences of mitochondrial cytochrome b gene of known reference animals and the biological material of unknown animal origin using software such as *Autoassembler/CLUSTAL X (1.8)*

↓

Identification of sequence from the aligned sequences that is homologous (or significantly similar) to the cytochrome b gene sequence of the DNA obtained from biological material of unknown animal origin.

↓

The species of homologous sequence would be the species of the biological material under investigation

↓

Application of the above information for the objectives mentioned in columns 7-13 under sub-heading 'Objective of invention' of heading 'Summary of invention'

Example 6:

The actual execution of the technique invented

As a first application and to demonstrate the ease and utility of this method, we investigated a case of forensic identification submitted at our laboratory to seek scientific opinion on animal hunting evidence. In this case, we received the half burned remains of an unknown animal, confiscated by the crime investigation agencies. The DNA was isolated from the above material following standard methods[74] and subjected to PCR amplification using the primers mentioned above (viz., 'mcb398' and 'mcb869'). Amplification reactions were carried out in 20 µl reaction volume containing 20 ηg of template DNA, 100µm each of dNTPs, 1.25 pmole of each primer, 1.5mM $MgCl_2$, 0.5 unit of Ampli*Taq* Gold (Perkin-Elmer-Cetus, USA) DNA polymerase and 1X PCR buffer *(10mM Tris-HCl, pH 8.3, and 50mM KCl). The amplification profiles followed were: an* initial denaturation at 95°C for 10 min, followed by 35 cycles each of denaturation at 95°C for 45 s, annealing at 51°C for 1 min, and extension at 72°C for 2 min. The extension step at 35th cycles was held for 10 min.

The PCR products obtained were sequenced in automated work station (ABI Prism 3700, PE-Biosystems) on both strands in triplicate and the sequence resolved (328 bp, shown in Figure 1a) was blasted against *mito* databases of NCBI using BLAST program[73]. The most significant alignment (bits Value 365, E value e^{-101}) of this sequence was produced with the cytochrome b gene sequence of *Felis catus*, (Table 3) indicating that species of

analyzed material belongs to family felidae. Further, the above sequence revealed from the confiscated remain was blasted against *nr* databases of NCBI using BLAST program. The most significant alignment (bits Value 603, E value e^{-170}) of this sequence was produced with the cytochrome b gene sequence of *Panthera pardus* (Table 4), indicating the identity of the analyzed material as that of a *Panthera pardus* source. Based on this information, we selected the reference animals listed in Table 5 representing different species and subspecies of felidae. The DNA isolated from reference animals was amplified and sequenced on both strands in triplicate using the primer pair mentioned above. Consensus sequences obtained were aligned using program *CLUSTAL X (1.8)* (Table 6). Sequence comparisons identified 113 variable sites in total amongst all animals analyzed (Table 7). Pair-vise comparisons of sequences were performed to find out the variation among different animals investigated. All the species investigated were differentiated by a their unique nucleotides sequences. The molecular signatures of different reference animals were compared with the molecular signature of the confiscated skin 'adil.flesh'. Table 7 demonstrate that the maximum similarity of the adil.flesh with 'gz11' i.e. known Leopard (*Panthera pardus*) species, indicating the identity of the adil.flesh, the confiscated skin, as that of a Panthera pardus origin. We also calculated the similarity matrix showing the pair-vise similarity amongst the animal species under investigation using *PHYLIP* software This matrix is shown in Table 8. It demonstrates that the animals belonging to different species had more variation; however, the animals of same species had maximum similarity among their cytochrome b sequences. The cytochrome b gene sequence of DNA isolated from confiscated material had maximum similarity with the sequences obtained from known Leopard source(99.7%, and 98.2 with 'gz11' and 'gz21', respectively); establishing the identity of the source of confiscated material as that of a Normal leopard (*Penthera pardus*) species. The step-vise procedure involved in above analysis is illustrated in Figure *1a, 1b and 1c, respectively.*

Thus, the primers invented by us can generate the molecular signature from any biological material of unknown animal origin, which actually is the characteristic of its family, genus and more precisely, the species. When these signatures are compared *in-silico* with the signatures already available in public databases (viz., GenBank, NCBI database etc) using *BLAST* software[73], it indicates identity of the family, genus or species of the analyzed material, which in turn is confirmed practically by comparing with the reference animals of the revealed family, genus or species, by including them in the further analysis by the primers 'mcb398' and 'mcb869'. Application of the information revealed could be in

fulfilling the requirements of objectives mentioned in columns 7-13 under sub-heading 'Objective of invention' of heading 'Summary of invention'

The method of the invention can be used to establish the identity of confiscated animal parts and products is one of the key requirements of wildlife identification in forensics. It is needed to establish the crime with the criminal beyond a reasonable doubt to avoid the human violation of wildlife resources. Various morphological biochemical and molecular approaches have been given for this purpose; however, none of the current methods is universally applicable to detect the mutilated animal remains of unknown origin. We have identified a fragment on the mitochondrial cytochrome b gene, which has enormous information to differentiate among various animal species back to the family, genus and species sources. We have also found that this fragment is flanked by the highly conserved sequences amongst a vast range of animal species. We invented a pair of universal primer that can amplify this fragment of DNA isolated from the biological material of an unknown animal origin in polymerase chain reaction (PCR) to reveal its identity at species and sub-species sources. This novel invention has great potential to revolutionize the whole scenario of wildlife forensic identification and crime investigation.

Table 1. The animal species included in the study for *in-silico* analysis

SN.	Code	Name	NCBI accession #	$P,S/F	$P,S/R
1	aep.mel	*Aepyceros melampus*	AF036289[1]	97, 60	94, 62
2	ore.ore	*Oreotragus oreotragus*	AF036288[1]	88, 52	94, 62
3	add.nas	*Addax nasomaculatus*	AF034722[2]	97, 60	95, 66
4	ory.dam	*Oryx damah*	AJ222685[1]	90, 58	95, 66
5	hip.equ	*Hippotragus equinus*	AF022060[3]	98, 63	85, 55
6	alc.bus	*Alcelaphus buselaphus*	AJ222681[1]	97, 60	98, 68
7	sig.lic	*Sigmoceros lichtensteinii*	AF034967[4]	97, 60	98, 68
8	bea.hun	*Beatragus hunteri*	AF034968[4]	97, 60	94, 62
9	dam.lun	*Damaliscus lunatus*	AF016635[3]	97, 60	77, 55
10	con.tau	*Connochaetes taurinus*	AF016638[3]	82, 56	93, 62
11	bis.bon	*Bison bonasus*	Y15005[5]	90, 58	87, 63
12	bos.gru	*Bos grunniens**	AF091631[6]	90, 58	94, 62
13	bos.tra	*Bos tragocamelus**	AJ222679[1]	90, 58	95, 66
14	buba.bub	*Bubalus bubalis**	D34637[7]	97, 60	93, 64
15	bub.min	*Bubalus mindorensis*	D82895[8]	97, 60	87, 62
16	tra.ang	*Tragelaphus angasii*	AF091633[6]	97, 60	87, 63
17	tra.eur	*Tragelaphus eurycerus*	AF036276[1]	90, 58	97, 64
18	nem.cau	*Nemorhaedus caudatus**	U17861[9]	95, 61	93, 59
19	pse.nay	*Pseudois nayaur*	AF034732[2]	89, 55	89, 59
20	amm.ler	*Ammotragus lervia*	AF034731[2]	94, 58	97, 63
21	cap.fal	*Capra falconeri**	D84202[10]	98, 63	95, 66
22	cap.ibe	*Capra ibex**	AF034735[2]	98, 63	89, 58
23	hem.jem	*Hemitragus jemlahicus**	AF034733[2]	95, 61	90, 61
24	rup.pyr	*Rupicapra pyrenaica*	AF034726[2]	95, 61	89, 59
25	rup.rup	*Rupicapra rupicapra*	AF034725[2]	95, 61	94, 64
26	pan.hod	*Pantholops hodgsoni*	AF034724[2]	98, 63	95, 66
27	bud.tax.tax	*Budorcas taxicolor taxicolor**	U17868[9]	90, 58	95, 66
28	ovi.amm	*Ovis ammon**	AF034727[2]	98, 63	97, 64
29	ovi.vig	*Ovis vignei**	AF034729[2]	98, 63	97, 64
30	cap.cri	*Capcornis crispus**	AJ304502[11]	98, 63	94, 63
31	ovi.mos	*Ovibos moschatus*	U17862[9]	98, 63	92, 61
32	ore.ame	*Oreamnos americanus*	AF190632[12]	98, 63	94, 62
33	cep.dor	*Cephalophus dorsalis*	AF091634[6]	97, 58	90, 61
34	cep.max	*Cephalophus maxwellii*	AF096629[13]	97, 60	88, 53
35	alc.alc	*Alces alces*	AJ000026[14]	95, 61	93, 59
36	hyd.ine	*Hydropotes inermis*	AJ000028[14]	97, 60	90, 63
37	mun.mun	*Muntiacus muntjak**	AF042718[15]	90, 58	93, 64
38	cer.ele.kan	*Cervus elaphus kansuensis**	AB021098[16]	98, 63	82, 59
39	cer.ele.xan	*Cervus elaphus xanthopygus**	AB021097[16]	98, 63	82, 59
40	cer.ele.can	*Cervus elaphus canadensis**	AB021096[16]	98, 63	90, 61
41	cer.nip.ce	*Cervus nippon centralis*	AB021094[16]	98, 63	90, 61
42	cer.nip.ye	*Cervus nippon yesoensis*	AB021095[16]	98, 63	90, 61
43	cer.nip.ke	*Cervus nippon keramae*	AB021091[16]	98, 63	90, 61

44	cer.nip.pu	*Cervus nippon pulchellus*	AB021090[16]	98, 63	90, 61
45	cer.nip.ni	*Cervus nippon nippon*	AB021093[16]	98, 63	90, 61
46	cer.ela.sc	*Cervus elaphus scoticus*	AB021099[16]	98, 63	90, 61
47	cer.dam	*Cervus dama*	AJ000022[14]	98, 63	88, 53
48	ran.tar	*Rangifer tarandus*	AJ000029[14]	98, 63	89, 57
49	mos.fus	*Moschus fuscus**	AF026888[17]	90, 59	90, 61
50	mos.leu	*Moschus leucogaster**	AF026889[17]	90, 59	90, 61
51	mos.chr	*Moschus chrysogaster**	AF026887[17]	90, 59	90, 61
52	mos.ber	*Moschus berezovskii**	AF026886[17]	90, 59	90, 61
53	mos.mos	*Moschus moschiferus**	AF026883[17]	90, 59	92, 61
54	kob.ell	*Kobus ellipsiprymnus*	AF022059[3]	91, 61	95, 66
55	kob.meg	*Kobus megaceros*	AJ222686[1]	91, 61	83, 56
56	red.aru	*Redunca arundinum*	AF096628[13]	91, 61	94, 62
57	red.ful	*Redunca fulvorufula*	AF036284[1]	89, 57	94, 62
58	neo.mos	*Neotragus moschatus*	AJ222683[1]	89, 57	94, 62
59	pel.cap	*Pelea capreolus*	AF022055[3]	91, 61	90, 61
60	ant.cer	*Antilope cervicapra**	AF022058[3]	82, 56	93, 64
61	sai.tat	*Saiga tatarica*	AF064487[18]	91, 61	92, 61
62	gaz.dam	*Gazella dama*	AF025954[3]	91, 61	92, 61
63	our.our	*Ourebia ourebi*	AF036288[1]	82, 56	82, 59
64	gaz.gaz	*Gazela gazella**	AJ222682[1]	91, 61	89, 57
65	rap.mel	*Raphicerus melanotis*	AF022053[3]	81, 54	80, 50
66	mad.kir	*Madoqua kirkii*	AF022070[3]	90, 58	97, 65
67	ant.ame	*Antilocapra americana*	AF091629[6]	98, 63	98, 68
68	tra.jav	*Tragulus javanicus**	D32189[19]	86, 57	86, 59
69	tra.nap	*Tragulus napu**	X56288[20]	81, 52	93, 58
70	bal.acu	*Balaenoptera acutorostrata*	X75753[21]	89, 56	97, 61
71	bal.bon	*Balaenoptera bonaerensis*	X75581[21]	89, 56	93, 59
72	bal.bor	*Balaenoptera borealis**	X75582[21]	89, 56	93, 59
73	bal.edi	*Balaenoptera edeni*	X75583[21]	89, 56	88, 54
74	esc.rob	*Eschrichtius robustus**	X75585[21]	97, 61	86, 57
75	bal.mus	*Balaenoptera musculus**	NC_001601[22]	97, 57	93, 59
76	meg.nov	*Megaptera novaeangliae**	X75584[21]	97, 61	94, 63
77	bal.phy	*Balaenoptera physalus**	NC_001321[23]	97, 57	94, 63
78	cap.mar	*Caperea marginata*	X75586[21]	93, 55	91, 53
79	cep.com	*Cephalorhynchus commersonii*	AF084073[24]	85, 51	88, 55
80	cep.eut	*Cephalorhynchus eutropia**	AF084072[24]	85, 51	92, 59
81	lag.obl	*Lagenorhynchus obliquidens*	AF084067[24]	94, 59	92, 59
82	cep.hea	*Cephalorhynchus heavisidii*	AF084070[24]	89, 56	97, 63
83	cep.hec	*cephalorhynchus hectori**	AF084071[24]	89, 56	92, 59
84	lag.aus	*Lagenorhynchus australis*	AF084069[24]	86, 54	92, 59
85	lag.cru	*Lagenorhynchus cruciger*	AF084068[24]	86, 54	92, 59
86	lag.obs	*Lagenorhynchus obscurus*	AF084066[24]	86, 54	92, 59
87	lis.bor	*Lissodelphis borealis*	AF084064[24]	85, 51	92, 59
88	lis.per	*Lissodelphis peronii*	AF084065[24]	86, 54	92, 59
89	glo.mac	*Globicephala macrorhynchus*	AF084055[24]	94, 59	88, 55
90	glo.mel	*Globicephala melas*	AF084056[24]	94, 59	88, 55
91	fer.att	*Feresa attenuata**	AF084052[24]	94, 59	92, 59

92	pep.ele	*Peponocephala electra**	AF084053[24]	94, 59	88, 55
93	gra.gri	*Grampus griseus*	AF084059[24]	97, 61	89, 59
94	pse.cra	*Pseudorca crassidens**	AF084057[24]	94, 59	92, 59
95	lag.acu	*Lagenorhynchus acutus*	AF084075[24]	98, 63	89, 59
96	orci.bre	*Orcinus orca*	AF084061[24]	86, 57	82, 52
97	orca.bre	*Orcaella brevirostris*	AF084063[24]	86, 57	91, 54
98	del.cap	*Delphinus capensis*	AF084087[24]	96, 54	97, 63
99	del.tro	*Delphinus tropicalis*	AF084088[24]	97, 57	97, 63
100	del.del	*Delphinus delphis*	AF084085[24]	97, 57	97, 63
101	sten.cly	*Stenella clymene*	AF084083[24]	97, 57	97, 63
102	sten.coe	*Stenella coeruleoalba*	AF084082[24]	97, 57	97, 66
103	tur.adu	*Tursiops aduncus*	AF084092[24]	97, 57	97, 63
104	sten.fro	*Stenella frontalis*	AF084090[24]	97, 57	97, 63
105	saus.chi	*Sousa chinensis*	AF084080[24]	97, 57	88, 59
106	sten.lon	*Stenella longirostris*	AF084103[24]	97, 61	97, 63
107	turs.tru	*Tursiops truncatus*	AF084095[24]	97, 57	96, 59
108	lage.alb	*Lagenorhynchus alborostris*	AF084074[24]	97, 61	97, 66
109	sten.bre	*Steno bredanensis*	AF084077[24]	97, 61	94, 64
110	sota.flu	*Sotalia fluviatilis*	AF304067[25]	97, 61	97, 63
111	del.leu	*Delphinapterus leucas*	U72037[26]	97, 61	95, 66
112	mono.mon	*Monodon monoceros*	U72038[26]	97, 61	95, 66
113	plat.gan	*Platanista gangetica**	AF304070[25]	97, 61	86, 59
114	plat.min	*Platanista minor**	X92543[27]	97, 61	86, 59
115	kogi.bre	*Kogia breviceps*	U72040[26]	97, 59	90, 63
116	kogi.sim	*Kogia simus*	AF304072[25]	96, 55	92, 63
117	phys.cat	*Physeter catodon*	AF304073[25]	97, 57	80, 58
118	lipo.vex	*Lipotes vexillifer**	AF304071[25]	89, 56	88, 53
119	phoc.sin	*phocoena sinus*	AF084051[24]	87, 49	92, 62
120	bera.bai	*Berardius bairdii*	X92541[27]	96, 55	90, 59
121	ziph.car	*Ziphius cavirostris*	X92540[27]	97, 61	89, 57
122	meso.eur	*Mesoplodon europaeus*	X92537[27]	97, 57	90, 61
123	meso.bid	*Mesoplodon bidens*	X92538[27]	97, 61	92, 61
124	meso.den	*Mesoplodon densirostris*	X92536[27]	91, 61	94, 63
125	hype.amp	*Hyperoodon ampullatus**	X92539[27]	97, 61	90, 65
126	meso.per	*Mesoplodon peruvianus*	AF304074[25]	97, 61	86, 58
127	pont.bla	*Pontoporia blainvillei*	AF304069[25]	92, 59	88, 55
128	hipp.amp	*Hippopotamus amphibius*	Y08813[29]	92, 58	95, 66
129	hex.lib	*Hexaprotodon liberiensis*	Y08814[29]	98, 63	97, 66
130	rhin.son	*Rhinoceros sondaicus**	AJ245725[30]	90, 59	87, 61
131	cera	*Ceratotherium simum*	NC_001808[32]	90, 59	90, 63
132	dic.sum	*Dicerorhinus sumatrensis*	AJ245723[30]	90, 59	86, 57
133	equu	*Equus asinus*	NC_001788[31]	91, 61	73, 51
134	baby.bab	*Babyrousa babyrussa*	Z50106[33]	89, 56	85, 56
135	phac.afr	*Phacochoerus africanus*	Z50090[33]	90, 59	87, 54
136	sus.scr.ew	*Sus scrofa haplotype EWB3**	AF136549[34]	97, 57	83, 54
137	sus.bar	*Sus barbatus*	Z50107[33]	97, 57	85, 55
138	lama.gla	*Lama glama*	U06429[33]	89, 55	85, 53
139	lama.gua	*lama guanicoe*	Y08812[29]	88, 54	86, 57

140	vic.vic	*Vicugna vicugna*	U06430[35]	89, 55	85, 53
141	cam.bac	*Camelus bactrianus*	U06427[35]	94, 58	86, 58
142	arc.for	*Arctocephalus forsteri*	X82293[36]	97, 60	87, 64
143	arc.gaz	*Arctocephalus gazella*	X82292[36]	94, 58	87, 64
144	eum.jub	*Eumetopias jubatus*	X82311[36]	97, 57	86, 57
145	zal.cal	*Zalophus californianus*	X82310[36]	89, 55	86, 57
146	odo.ros	*Odobenus rosmarus*	X82299[36]	91, 61	81, 52
147	pho.vit	*Phoca vitulina*	X82306[36]	90, 58	87, 64
148	pho.fascia	*Phoca fasciata*	X82302[36]	98, 63	95, 66
149	pho.gro	*Phoca groenlandica*	X82303[36]	92, 59	90, 61
150	cys.cri	*Cystophora cristata*	X82294[36]	89, 56	87, 64
151	hyd.lep	*Hydrurga leptonyx*	X82297[36]	89, 55	82, 54
152	lep.wed	*Leptonychotes weddelli*	X72005[37]	98, 63	91, 66
153	mir.leo	*Mirounga leonina*	X82298[36]	89, 55	82, 59
154	eri.bar	*Erignathus barbatus*	X82295[36]	89, 56	87, 63
155	mon.sch	*Monachus schauinslandi*	X72209[37]	91, 61	87, 60
156	hela.mal	*Helarctos malayanus* *	U18899[38]	84, 54	90, 63
157	sel.thi	*Selenarctos thibetanus* *	AB020910[39]	89, 57	87, 64
158	ail.ful	*Ailurus fulgen*s*	X94919[40]	93, 55	87, 64
159	fel	*Felis catus*	NC_001700[41]	85, 56	90, 63
160	can	*Canis familiaris*	NC_002008[42]	98, 58	84, 54
161	tal	*Talpa europaea*	NC_002391[43]	81, 50	92, 57
162	gla.sab	*Glaucomys sabrinus*	AF011738[44]	90, 59	82, 54
163	gla.vol	*Glaucomys volans*	AB030261[45]	90, 59	87, 60
164	hyl.pha	*Hylopetes phayrei* *	AB030259[45]	91, 61	81, 50
165	pet.set	*Petinomys setosus* *	AB030260[45]	91, 61	81, 50
166	bel.pea	*Belomys pearsonii* *	AB030262[45]	91, 61	87, 64
167	pte.mom	*Pteromys momonga* *	AB030263[45]	97, 61	90, 63
168	gala.demi	*Galagoides demidoff*	AF271411[46]	97, 58	87, 64
169	pero.pot	*Perodicticus potto*	AF271413[46]	97, 60	87, 63
170	gala.mat	*Galago matschiei*	AF271409[46]	97, 60	90, 61
171	gala.moh	*Galago moholi*	AF271410[46]	97, 57	95, 66
172	oto.gar	*Otolemur garnettii*	AF271412[46]	92, 58	87, 60
173	lor.tar	*Loris tardigradus* *	U53581[47]	97, 60	93, 59
174	nyc.cou	*Nycticebus coucang* *	U53580[47]	97, 60	95, 66
175	mus	*Mus musculus*	NC_001569[48]	97, 60	86, 59
176	gorr	*Gorilla gorilla*	NC_001645[49]	89, 57	80, 58
177	homo	*Homo sapiens sapiens*	NC_001807[50]	96, 55	84, 64
178	dug.dug	*Dugong dugong* *	U07564[51]	97, 60	89, 59
179	ele.max	*Elephas maximus* *	AB002412[52]	97, 60	76, 57
180	afr.con	*Afropavo congensis*	AF013760[53]	97, 58	87, 63
181	pavo.mut	*Pavo muticus* *	AF013763[53]	97, 57	87, 63
182	tra.bly	*Tragopan blythii* *	AF200722[54]	89, 55	85, 57
183	tra.sat	*Tragopan satyra* *	AF229837[54]	89, 55	86, 61
184	tra.cob	*Tragopan caboti*	AF200723[54]	89, 55	86, 61
185	tra.tem	*Tragopan temminckii* *	AF028802[55]	89, 55	81, 56
186	arg.arg	*Argusianus argus*	AF013761[53]	89, 55	87, 63
187	cat.wal	*Catreus wallichi* *	AF028792[55]	88, 54	85, 57

188	cro.cro	*Crossoptilon crossoptilon**	AF028794[53]	89, 55	85, 57
189	sym.ree	*Syrmaticus reevesi**	AF028801[53]	89, 55	85, 57
190	bam.tho	*Bambusicola thoracica**	AF028790[53]	80, 48	94, 64
191	fra.fra	*Francolinus francolinus*	AF013762[53]	97, 58	86, 61
192	ith.cru	*Ithaginis cruentus**	AF068193[53]	98, 63	85, 57
193	ant.par	*Anthropoides paradisea*	U27557[56]	85, 56	82, 58
194	ant.vir	*Anthropoides virgo*	U27545[56]	84, 54	82, 52
195	gru.ant.an	*Grus antigone antigone*	U11060[57]	90, 58	87, 63
196	gru.ant.gi	*Grus antigone gillae*	U11064[57]	90, 58	87, 63
197	gru.any.sh	*Grus antigone sharpei*	U11061[57]	90, 58	87, 63
198	gru.leu	*Grus leucogeranus**	U27549[56]	90, 58	87, 63
199	gru.can.pr	*Grus canadensis pratensis*	U27553[56]	97, 60	87, 63
200	gru.can.ro	*Grus canadensis rowani*	U27552[56]	97, 60	87, 63
201	gru.can.ta	*Grus canadensis tabida*	U27551[56]	98, 63	87, 63
202	gru.can.ca	*Grus canadensis canadensis*	U27554[56]	97, 61	87, 63
203	gru.ame	*Grus americana*	U27555[56]	90, 58	87, 63
204	gru.gru	*Grus grus*	U27546[56]	89, 54	87, 63
205	gru.mon	*Grus monacha**	U27548[56]	90, 58	87, 63
206	gru.nig	*Grus nigricollis**	U27547[56]	90, 58	87, 63
207	gru.jap	*Grus japonensis*	U27550[56]	81, 54	87, 63
208	cic.boy	*Ciconia boyciana**	NC_002196[58]	94, 58	79, 60
209	rhe.ame	*Rhea americana*	AF090339[59]	93, 63	79, 60
210	ant.alb	*Anthracoceros albirostris**	U89190[60]	97, 61	86, 59
211	fal.fam	*Falco femoralis*	U83310[61]	97, 61	86, 60
212	fal.ver	*Falco verpertinus*	U83311[61]	97, 61	85, 57
213	fal.par	*Falco peregrinus**	U83307[61]	97, 61	84, 52
214	fal.spa	*Falco sparverius*	U83306[61]	92, 59	80, 51
215	ayt.ame	*Aythya americana*	NC_000877[62]	98, 63	94, 62
216	smi.sha	*Smithornis sharpei*	NC_000879[59]	97, 58	90, 61
217	vid.cha	*Vidua chalybeata*	NC_000880[59]	97, 60	87, 64
218	chry.pic	*Chrysemys picta*	NC_002073[63]	89, 56	86, 57
219	emy.orb.ku	*Emys orbicularis*	AJ131425[64]	90, 59	94, 63
220	che.mud	*Chelonia mydas**	AB012104[65]	90, 58	94, 63
221	eum.egr	*Eumeces egregius*	AB016606[65]	86, 55	73, 51

Table 2. Multiple sequence alignment of 472 bp fragment of mitochondrial cytochrome b gene of 221 animal species

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PRIMER 'mcb393'   TACCATGAGGACAAATATCATTCTG
                  * ** ** ** ** ** ** ** ** * * ** ** ** ** ** * ** **
aep.mel           TGCCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACAAATCTCCTCTCAGCAA 60
ore.ore           TTCCGTGAGGACAAATATCATTTTGAGGGGCTACAGTCATTACTAATCTCCTCTCAGCAA 60
add.nas           TGCCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATCACCAACCTTCTCTCAGCAA 60
ory.dam           TACCATGAGGACAAATATCATTTTGAGGGGCAACAGTTATCACTAACCTTCTCTCAGCAA 60
hip.equ           TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATCACCAACCTCCTCTCAGCAA 60
alc.bus           TGCCATGAGGACAAATATCATTCTGAGGGGCAACAGTCATCACCAATCTCCTCTCAGCAA 60
sig.lic           TGCCATGAGGACAAATATCATTCTGAGGGGCAACAGTCATCACCAATCTCCTCTCAGCAA 60
bea.hun           TGCCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATCACCAACCTCCTCTCAGCAA 60
dam.lun           TGCCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATCACTAACCTCCTCTCAGCAA 60
con.tau           TACCATGAGGACAAATATCCTTTTGAGGAGCAACAGTCATCACCAACCTCCTCTCAGCAA 60
amm.ler           TGCCATGAGGACAGATATCATTCTGAGGGGCAACAGTCATCACCAACCTTCTCTCAGCAA 60
pse.nay           TGCCATGAGGACAAATATCATTTTGAGGGGCAACAGTCATCACTAACCTTCTCTCAGCAA 60
cap.ibe           TACCATGAGGACAAATATCATTCTGAGGGGCAACAGTCATCACCAACCTTCTCTCAGCAA 60
hem.jem           TACCATGAGGACAGATATCATTCTGAGGGGCAACAGTCATCACCAATCTCCTCTCAGCAA 60
cap.fal           TACCATGAGGACAAATATCATTCTGAGGGGCAACAGTTATTACCAATCTCCTCTCAGCAA 60
rup.pyr           TACCATGAGGACAGATATCATTCTGAGGAGCAACAGTTATTACCAACCTCCTCTCAGCGA 60
rup.rup           TACCATGAGGACAGATATCATTCTGGGGAGCAACAGTTATTACCAATCTTCTCTCAGCAA 60
nem.cau           TACCATGAGGACAGATATCATTCTGAGGGGCAACAGTTATTACCAACCTCCTCTCAGCAA 60
bud.tax.tax       TACCATGAGGACAAATATCATTTTGAGGAGCAACAGTCATTACCAACCTCCTTTCAGCAA 60
pan.hod           TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTAATTACCAACCTCCTTTCAGCAA 60
ovi.amm           TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTTATTACCAACCTCCTTTCAGCAA 60
ovi.vig           TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTTATTACCAACCTCCTTTCAGCAA 60
cap.cri           TACCATGAGGACAAATATCATTCTGAGGGGCTACAGTCATTACTAACCTCCTCTCAGCAA 60
ovi.mos           TACCATGAGGACAAATATCATTCTGAGGAGCTACAGTCATCACTAACCTCCTCTCAGCAA 60
ore.ame           TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAATCTCCTTTCAGCAA 60
cep.dor           TCCCATGAGGGCAAATATCATTCTGAGGAGCCACAGTCATTACCAACCTCCTCTCAGCAA 60
cep.max           TCCCATGAGGACAAATATCATTCTGAGGAGCCACAGTCATTACCAACCTCCTCTCAGCAA 60
bis.bon           TACCATGAGGACAAATATCATTTTGAGGAGCAACAGTCATTACCAACCTCCTATCAGCAA 60
bos.gru           TACCATGAGGACAAATATCATTTTGAGGGGCAACAGTCATTACCAACCTCCTATCAGCAA 60
bos.tra           TACCATGAGGACAAATATCATTTTGAGGAGCAACAGTTATTACCAATCTATTATCAGCAA 60
bub.min           TGCCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATCACCAACCTTCTCTCAGCAA 60
buba.bub          TGCCATGAGGACAAATATCATTCTGAGGGGCAACAGTCATCACCAACCTTCTCTCAGCAA 60
tra.ang           TGCCATGAGGACAAATATCATTCTGAGGAGCAACGGTCATCACAAACCTCCTATCAGCAA 60
tra.eur           TACCATGAGGACAAATATCATTTTGAGGAGCAACAGTCATCACAAACCTTCTATCAGCAA 60
kob.ell           TACCATGAGGACAAATATCCTTCTGAGGAGCAACAGTCATCACCAATCTCCTTTCAGCAA 60
kob.meg           TACCATGAGGACAAATATCCTTCTGAGGAGCGACAGTCATCACTAATCTCCTTTCAGCAA 60
red.aru           TACCATGAGGACAAATATCCTTCTGAGGAGCAACAGTTATCACTAATCTTCTCTCAGCAA 60
red.ful           TGCCATGGGGACAAATATCCTTCTGAGGAGCAACAGTTATCACTAACCTTCTCTCAGCAA 60
neo.mos           TGCCATGGGGACAAATATCCTTCTGAGGAGCAACAGTCATCACCAATCTACTATCAGCAA 60
pel.cap           TACCATGAGGACAAATATCCTTCTGAGGAGCAACAGTCATCACCAACCTTCTCTCAGCAA 60
gaz.dam           TACCATGAGGACAAATATCTTTCTGAGGGGCAACAGTTATCACTAACCTCCTCTCAGCAA 60
our.our           TACCATGAGGACAAATATCCTTTTGAGGAGCAACAGTCATCACCAACCTCCTCTCAGCAA 60
ant.cer           TACCATGAGGACAAATATCTTTTTGAGGAGCAACAGTCATCACCAATCTCCTTTCAGCAA 60
sai.tat           TACCATGAGGACAAATATCTTTCTGAGGAGCAACAGTCATCACCAATCTCCTTTCAGCAA 60
mad.kir           TGCCATGAGGACAAATATCCTTCTGAGGAGCAACAGTTATCACTAACCTCCTCTCAGCAA 60
rap.mel           TACCATGGGGACAAATATCCTTTTGAGGAGCAACAGTCATCACTAATCTCCTCTCAGCAA 60
gaz.gaz           TACCATGAGGACAAATATCTTTCTGAGGAGCAACAGTTATCACTAACCTCCTCTCAGCAA 60
ant.ame           TACCATGAGGACAAATATCATTCTGAGGGGCAACAGTCATTACTAACCTACTCTCAGCAA 60
hyd.ine           TTCCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACTAATCTCCTCTTTCAGCAA 60
mun.mun           TACCATGAGGACAAATATCATTTTGAGGAGCAACAGTCATTACTAACCTCCTCTTTCAGCAA 60
alc.alc           TACCATGAGGACAGATATCATTCTGAGGGGCAACAGTCATTACTAACCTCCTCTCAGCAA 60
cer.ela kun       TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA 60
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cer.ela.xan     TACCATGAGGACAAATATCATTCTGAGGAGCAACGGTCATTACCAACCTTCTCTCAGCAA 60
cer.ela.can     TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA 60
cer.nip.cent    TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTCCTCTCAGCAA 60
cer.nip.yes     TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTCCTCTCAGCAA 60
cer.nip.ker     TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA 60
cer.nip.pul     TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA 60
cer.nip.nip     TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTCCTCTCAGCAA 60
cer.ela.sco     TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATCACCAACCTTCTCTCAGCAA 60
cer.dam         TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTTATTACCAATCTTCTCTCAGCAA 60
ran.tar         TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTTATCACAAACCTCCTCTCAGCAA 60
mos.fus         TACCTTGAGGACAAATATCTTTCTGAGGAGCGACAGTTATTACCAATCTTCTCTCAGCAA 60
mos.leu         TACCTTGAGGACAAATATCTTTCTGAGGAGCAACAGTTATTACCAATCTTCTCTCAGCAA 60
mos.chr         TACCTTGAGGACAAATATCTTTCTGAGGAGCAACAGTTATTACCAATCTTCTCTCAGCAA 60
mos.ber         TACCTTGAGGACAAATATCTTTCTGAGGAGCAACAGTTATTACCAATCTTCTCTCAGCAA 60
mos.mos         TACCTTGAGGACAAATATCTTTCTGAGGAGCAACAGTCATCACTAACCTTCTCTCAGCAA 60
tra.jav         TACCCTGAGGACAGATATCTTTCTGAGGAGCCACAGTCATCACCAACCTCTTATCAGCTA 60
trag.nap        TACCCTGAGGGCAAATATCTTTTTGAGGAGCTACAGTCATCACTAACCTTCTTTCAGCAA 60
bala.acu        TACCCTGAGGACAAATATCATTTTGAGGTGCAACCGTCATCACCAACCTCCTATCAGCAA 60
bala.bon        TACCCTGAGGACAAATATCATTTTGAGGCGCAACCGTCATCACCAACCTCCTATCAGCAA 60
bala.bor        TACCCTGAGGACAAATATCATTTTGAGGCGCAACCGTCATCACCAACCTCTTATCAGCAA 60
bala.edi        TACCCTGAGGACAAATATCATTTTGAGGCGCAACCGTCATCACCAACCTCTTATCAGCAA 60
esch.rob        TACCCTGAGGACAAATATCATTCTGAGGCGCAACCGTTATCACCAACCTCCTATCAGCAA 60
bala.mus        TGCCCTGAGGACAAATATCATTCTGAGGCGCAACCGTCATCACCAACCTCCTATCAGCAA 60
mega.nov        TACCCTGAGGACAAATATCATTCTGAGGCGCAACCGTCATCACCAACCTTCTATCAGCAA 60
bala.phy        TGCCCTGAGGACAAATATCATTCTGAGGCGCAACTGTAATCACTAACCTCCTATCAGCAA 60
cap.mar         TGCCCTGAGGACAGATATCATTCTGAGGCGCAACCGTCATCACCAACCTCCTATCAGCAA 60
ceph.com        TACCCTGGGGACAGATATCATTTTGAGGTGCAACAGTCATCACCAACCTCCTATCAGCAA 60
ceph.eut        TACCCTGGGGACAGATATCATTTTGAGGTGCAACAGTCATCACCAACCTCCTATCAGCAA 60
lage.obl        TACCCTGAGGACAGATATCATTCTGAGGTGCAACAGTCATCACCAACCTCCTATCAGCAA 60
ceph.hea        TACCCTGAGGACAAATATCATTTTGAGGCGCAACAGTCATCACCAACCTCCTATCAGCAA 60
ceph.hec        TACCCTGAGGACAAATATCATTTTGAGGTGCAACAGTCATCACCAACCTCCTATCAGCAA 60
lage.aus        TACCCTGAGGACAGATATCATTTTGAGGTGCAACAGTCATCACCAACCTCCTATCAGCAA 60
lage.cru        TACCCTGAGGACAGATATCATTTTGAGGTGCAACAGTCATCACCAACCTCCTATCAGCAA 60
lage.obs        TACCCTGAGGACAGATATCATTTTGAGGTGCAACAGTCATCACCAACCTCCTATCAGCAA 60
lisso.bor       TACCCTGAGGGCAGATATCATTTTGAGGTGCAACCGTCATCACCAACCTCCTATCAGCAA 60
lisso.per       TACCCTGAGGACAGATATCATTCTGAGGCGCAACCGTCATCACCAATCTCCTATCAGCAA 60
glo.mac         TACCCTGAGGACAGATATCATTCTGAGGCGCAACCGTCATCACCAATCTCCTATCAGCAA 60
glo.mel         TACCCTGAGGACAGATATCATTCTGAGGCGCAACCGTCATCACCAATCTCCTATCAGCAA 60
fere.att        TACCCTGAGGACAGATATCATTCTGAGGCGCAACCGTCATCACCAATCTCCTATCAGCAA 60
pepo.ele        TACCCTGAGGACAGATATCATTCTGAGGCGCAACCGTCATCACCAATCTCCTATCAGCAA 60
gram.gri        TACCCTGAGGACAAATATCATTCTGAGGCGCAACCGTCATCACCAATCTCCTATCAGCAA 60
pse.cra         TACCCTGAGGACAGATATCATTCTGAGGCGCAACCGTCATCACCAATCTTCTATCAGCAA 60
lage.acu        TACCATGAGGACAAATATCATTCTGAGGCGCAACCGTTATCACCAATCTCCTATCAGCAA 60
orci.bre        TACCCTGAGGACAGATATCTTTCTGAGGCGCAACCGTCATTACTAATCTCCTATCAGCAA 60
crca.bre        TACCCTGAGGACAGATATCCTTCTGAGGTGCAACCGTCATCACCAATCTCCTATCAGCAA 60
del.cap         TGCCCTGGGGACAAATATCATTCTGAGGCGCAACCGTCATCACCAACCTCTTATCAGCAA 60
del.tro         TGCCCTGAGGACAAATATCATTCTGAGGCGCAACCGTCATCACCAACCTCTTATCAGCAA 60
del.del         TGCCCTGAGGACAAATATCATTCTGAGGCGCAACCGTCATCACCAACCTCTTATCAGCAA 60
sten.cly        TGCCCTGAGGACAAATATCATTCTGAGGCGCAACCGTCATCACCAACCTCCTATCAGCAA 60
sten.coe        TGCCCTGAGGACAAATATCATTCTGAGGCGCAACCGTCATCACCAACCTCTTATCAGCAA 60
tur.adu         TGCCCTGAGGACAAATATCATTCTGAGGCGCAACCGTCATCACCAACCTCTTATCAGCAA 60
sten.fro        TGCCCTGAGGACAAATATCATTCTGAGGCGCAACCGTCATCACCAACCTCTTATCAGCAA 60
saus.chi        TGCCCTGAGGACAAATATCATTCTGAGGCGCAACCGTTATCACCAACCTCCTATCAGCAA 60
sten.lon        TACCCTGAGGACAAATATCATTCTGAGGTGCAACCGTCATCACCAACCTCCTATCAGCAA 60
turs.tru        TGCCCTGAGGACAAATATCATTCTGAGGCGCAACCGTCATCACCAACCTCTTATCAGCAA 60
lage.alb        TACCCTGAGGACAAATATCATTCTGAGGCGCAACCGTCATCACTAATCTCCTATCAGCAA 60
sten.bre        TACCCTGAGGACAAATATCATTCTGAGGTGCAACCGTCATTACCAACCTCCTGTCAGCAA 60
sota.flu        TACCCTGAGGACAAATATCATTCTGAGGCGCAACCGTCATTACCAATCTCCTATCAGCAA 60
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lipo.vex         TACCCTGAGGACAAATATCATTTTGAGGCGCAACCGTCATCACTAATCTTCTATCAGCAA 60
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meso.per         TACCTTGAGGACAAATATCATTCTGAGGCGCAACTGTCATTACTAATCTTTTATCTGCTA 60
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zal.cal          TTCCATGAGGACAAATATCATTTTGAGGAGCAACCGTCATTACCAACCTCCTATCAGCAG 60
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pho.gro          TACCATGAGGGCAAATGTCATTCTGAGGAGCAACAGTTATCACTAATCTACTATCAGCAA 60
pho.vit          TACCATGAGGACAAATATCATTTTGAGGAGCAACAGTCATCACCAATCTACTATCAGCAA 60
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hyd.lep          TGCCATGAGGACAAATATCATTTTGAGGAGCAACCGTTATTACCAACTTACTATCAGCAA 60
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nyc.cou         TCCCATGAGGACAAATATCATTCTGAGGTGCCACCGTCATCACTAACCTACTATCGGCAA 60
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tra.bly         TCCCATGAGGACAAATATCATTTTGAGGGGCTACCGTCATCACAAACTTATTCTCAGCAA 60
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gru.leu         TACCATGAGGACAAATATCATTTTGAGGGGCTACAGTCATCACCAATCTCTTCTCAGCCG 60
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rhe.ame         TACCATGAGGACAAATATCATTCTGAGGAGCTACAGTTATTACCAACCTATTCTCAGCCA 60
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smi.sha         TCCCATGAGGCCAAATATCATTCTGAGGTGCTACAGTAATCACCAACCTCTTCTCAGCTA 60
vid.cha         TGCCATGAGGACAAATATCATTCTGAGGAGCCACAGTAATCACAAACCTATTCTCAGCAA 60
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eum.egr         TCCCATGGGGACAGATATCCTTCTGAGGGCAATCGTAATTACAAACCTATTATCAGCAA 60
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ceph.hec    TCCCCTACATCGGCACTACCTTAGTAGAATGAATCTGAGGAGGATTTTCCGTAGATAAAG 120
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saus.chi    TCCCTTACATTGGCACTACCCTAGTTGAATGAATCTGAGGTGGATTTTCCGTAGACAAAG 120
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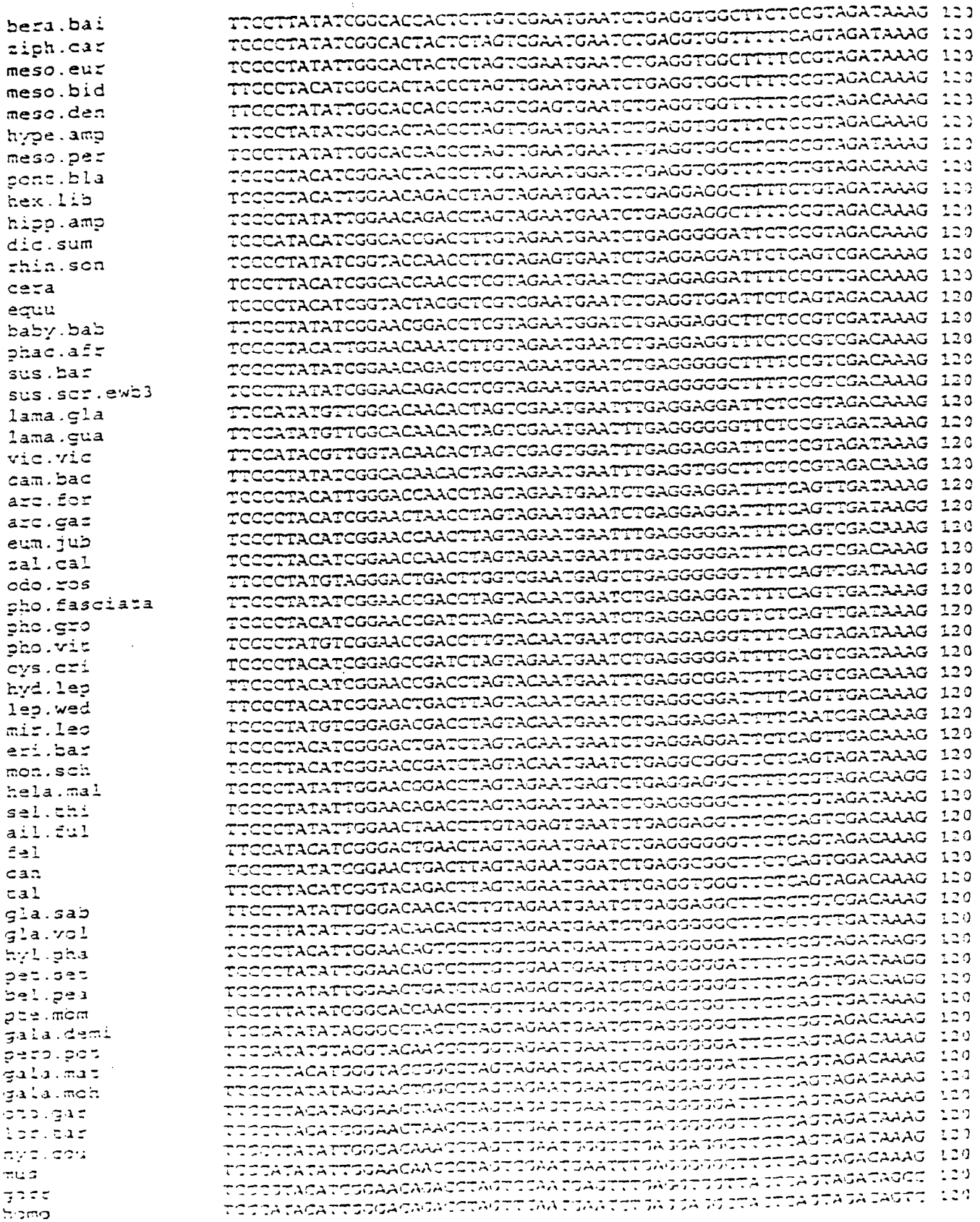

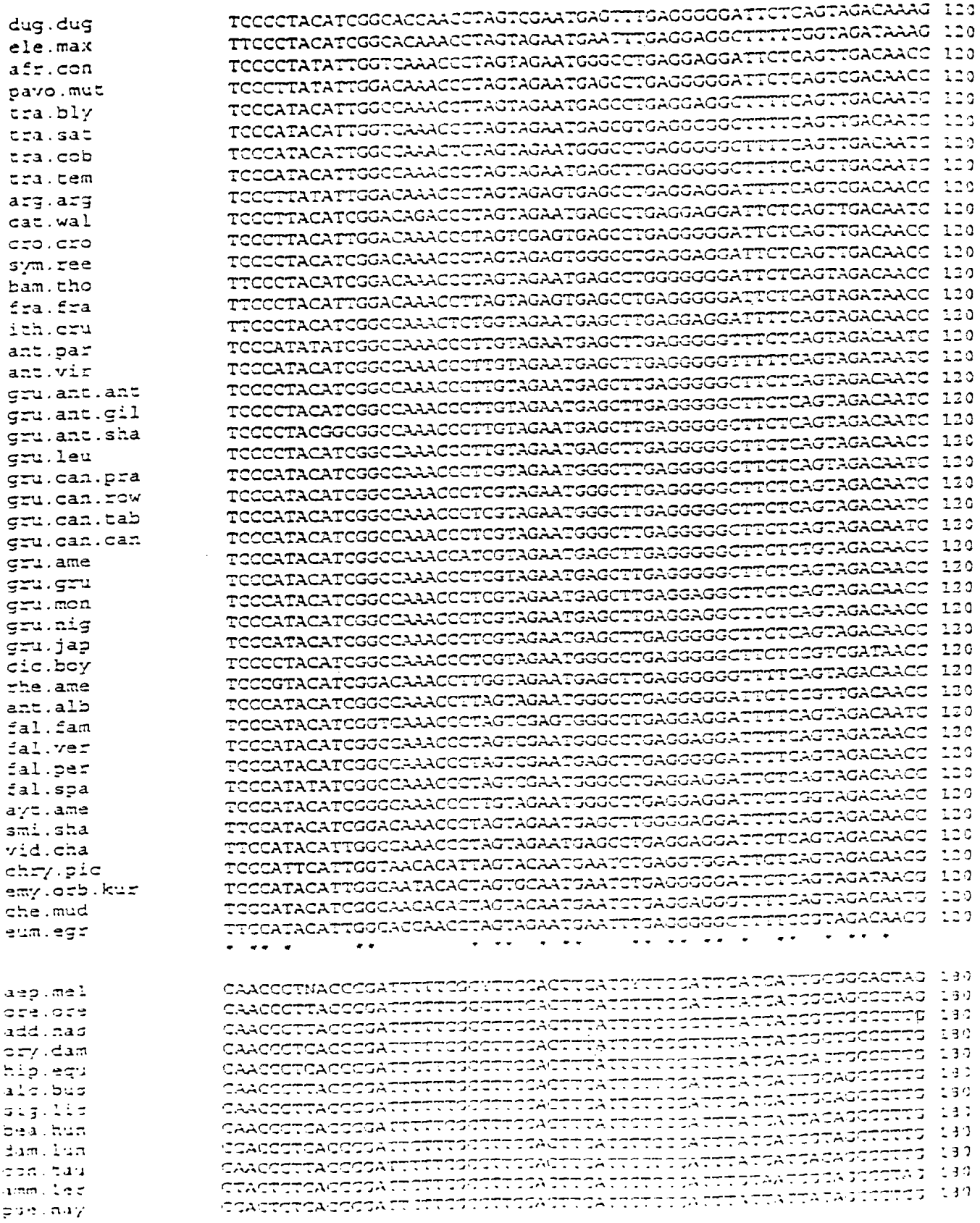

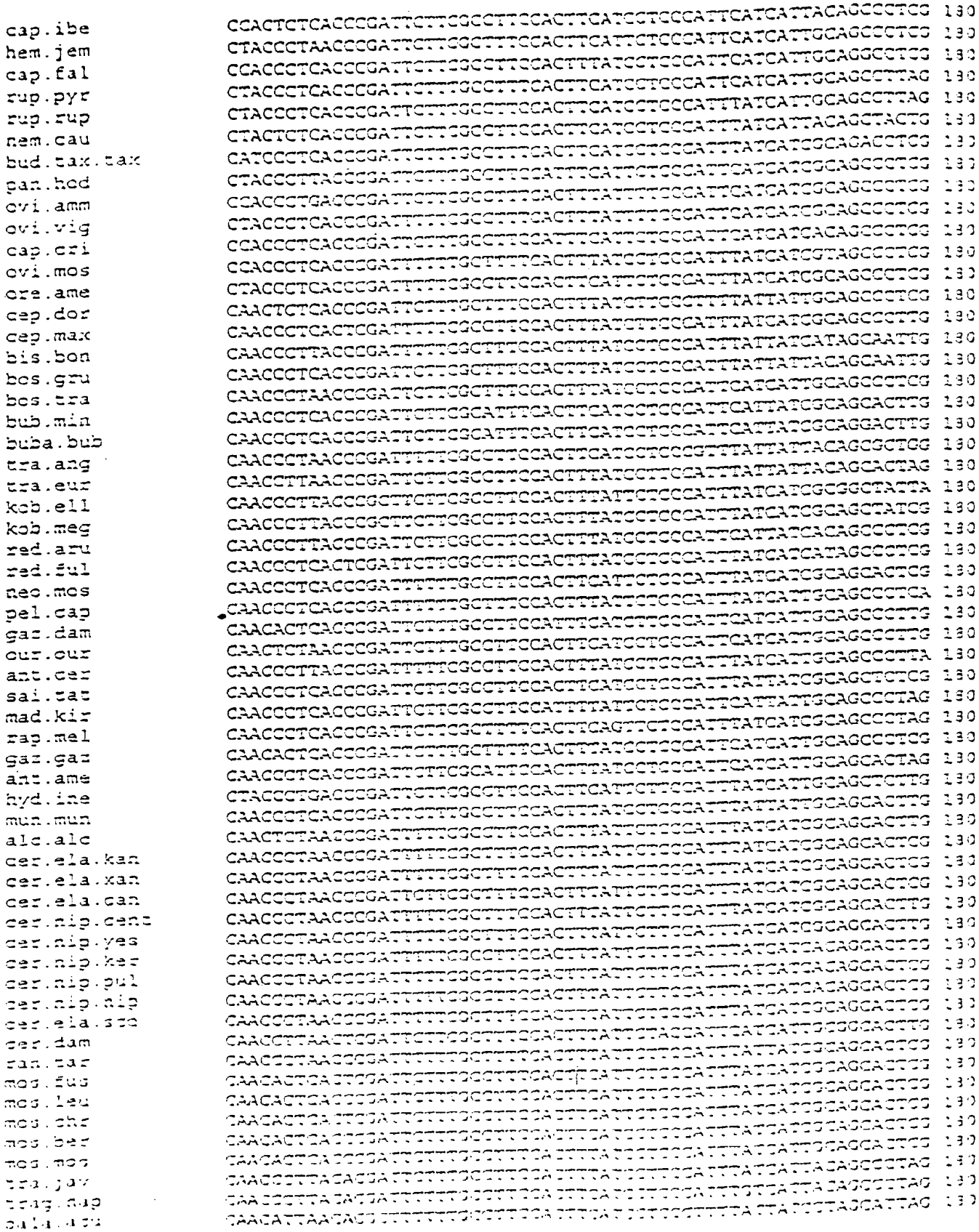

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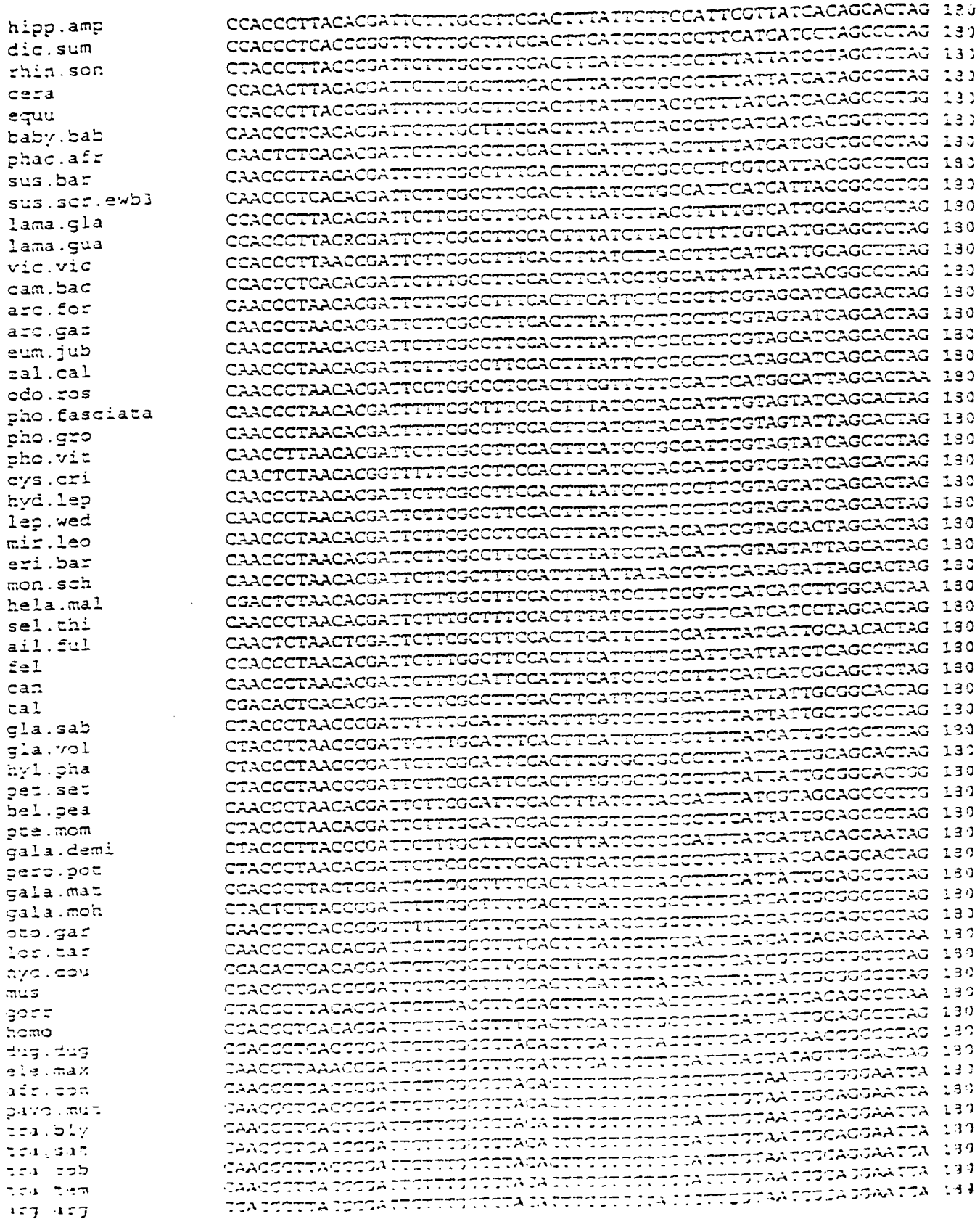

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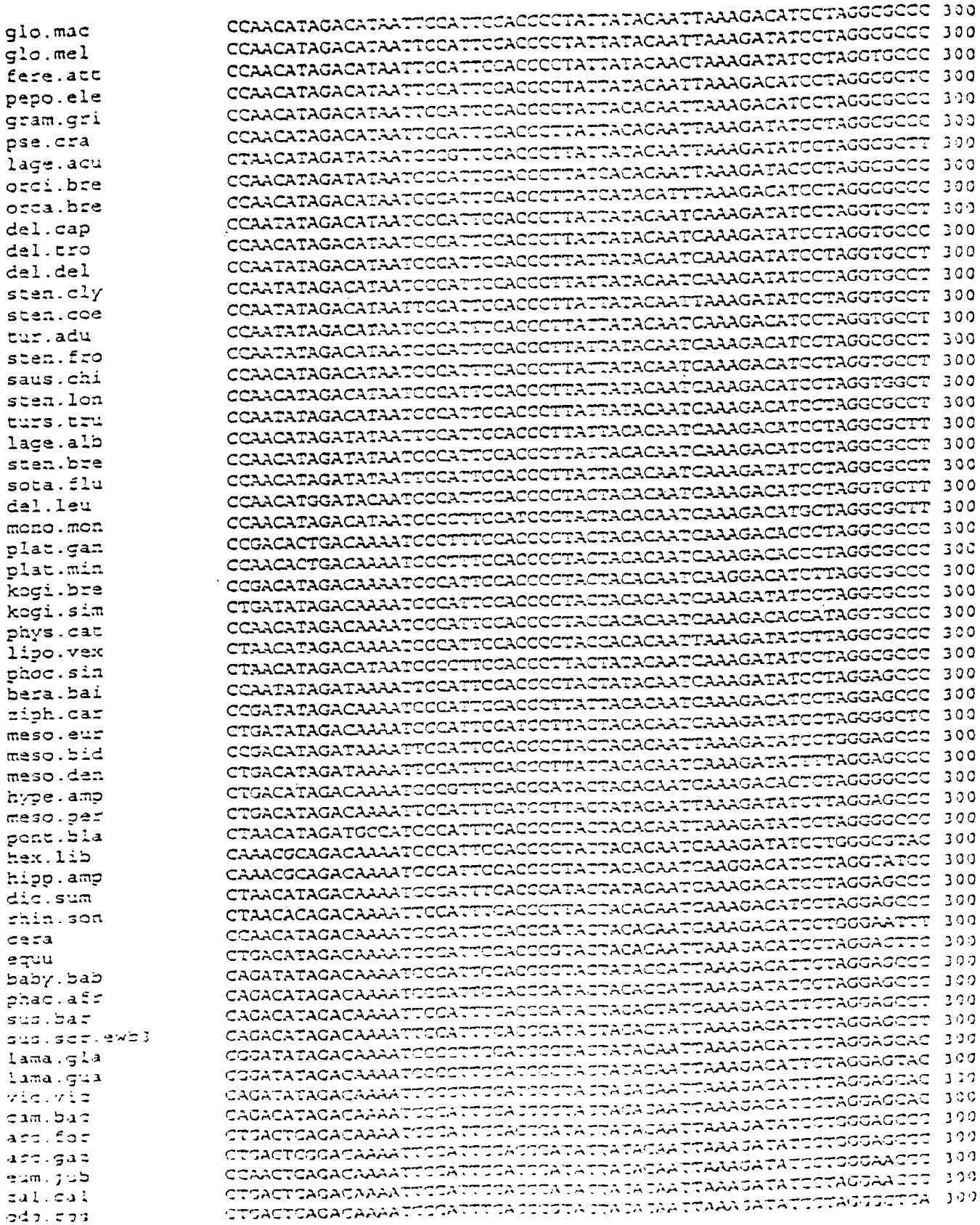

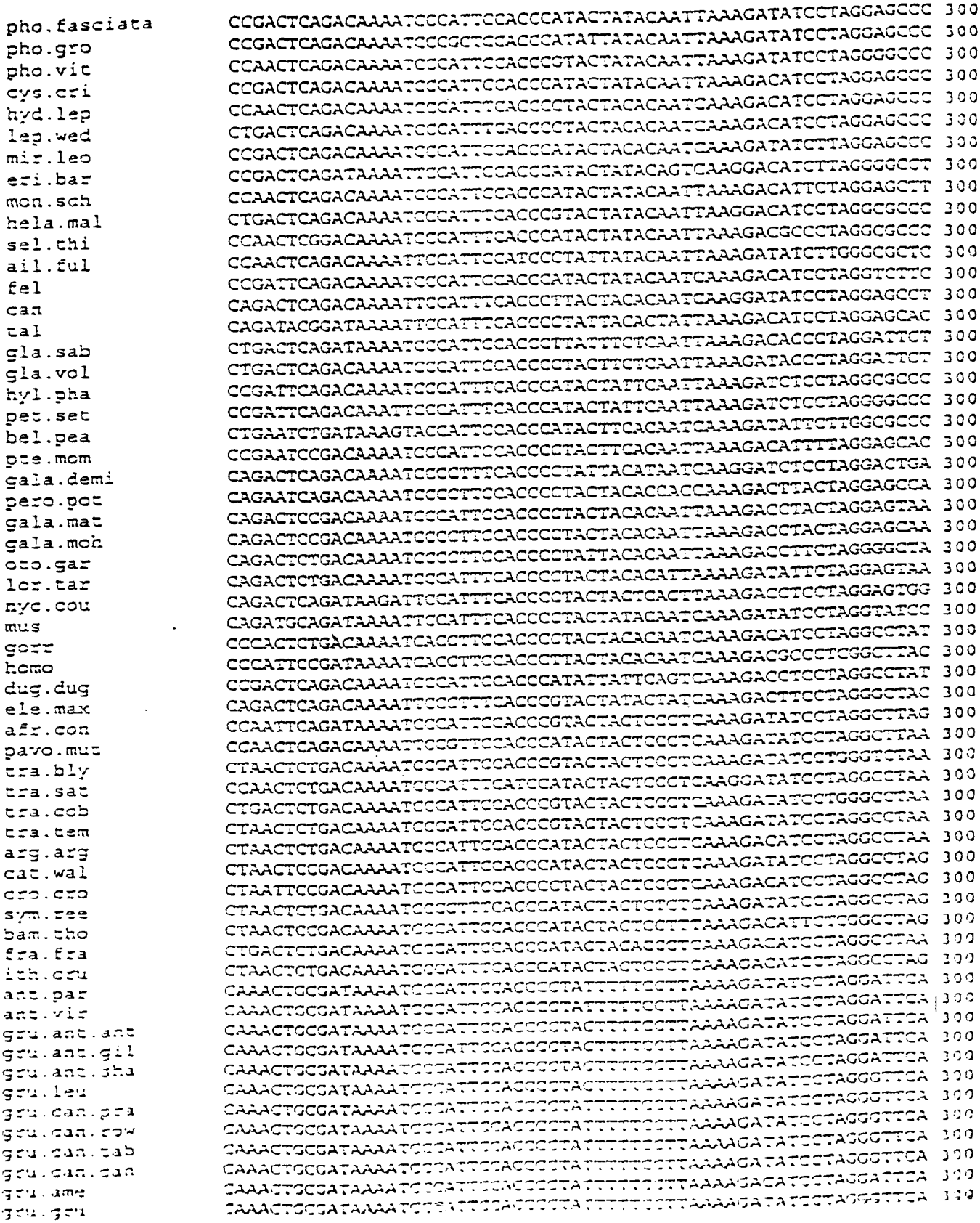
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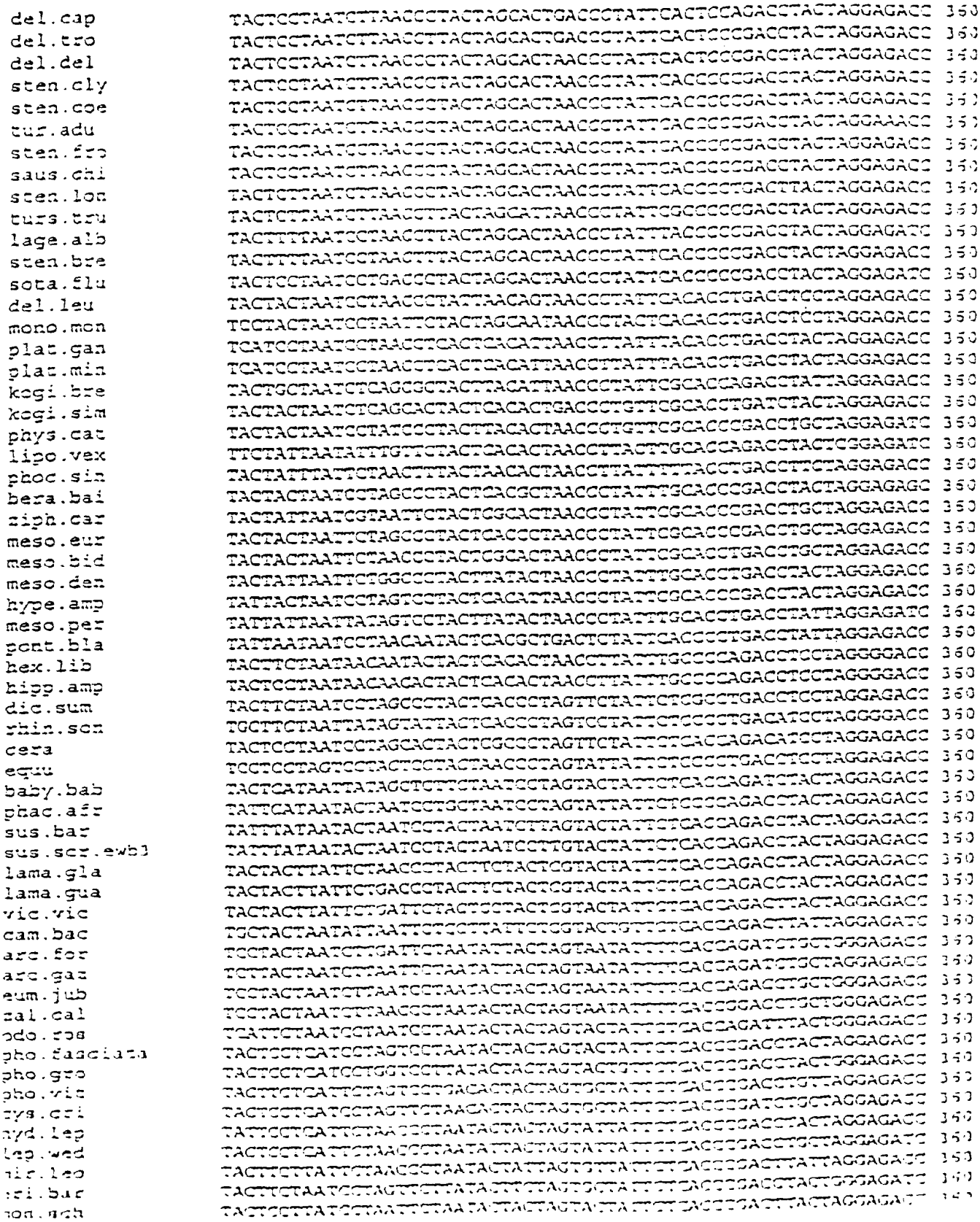
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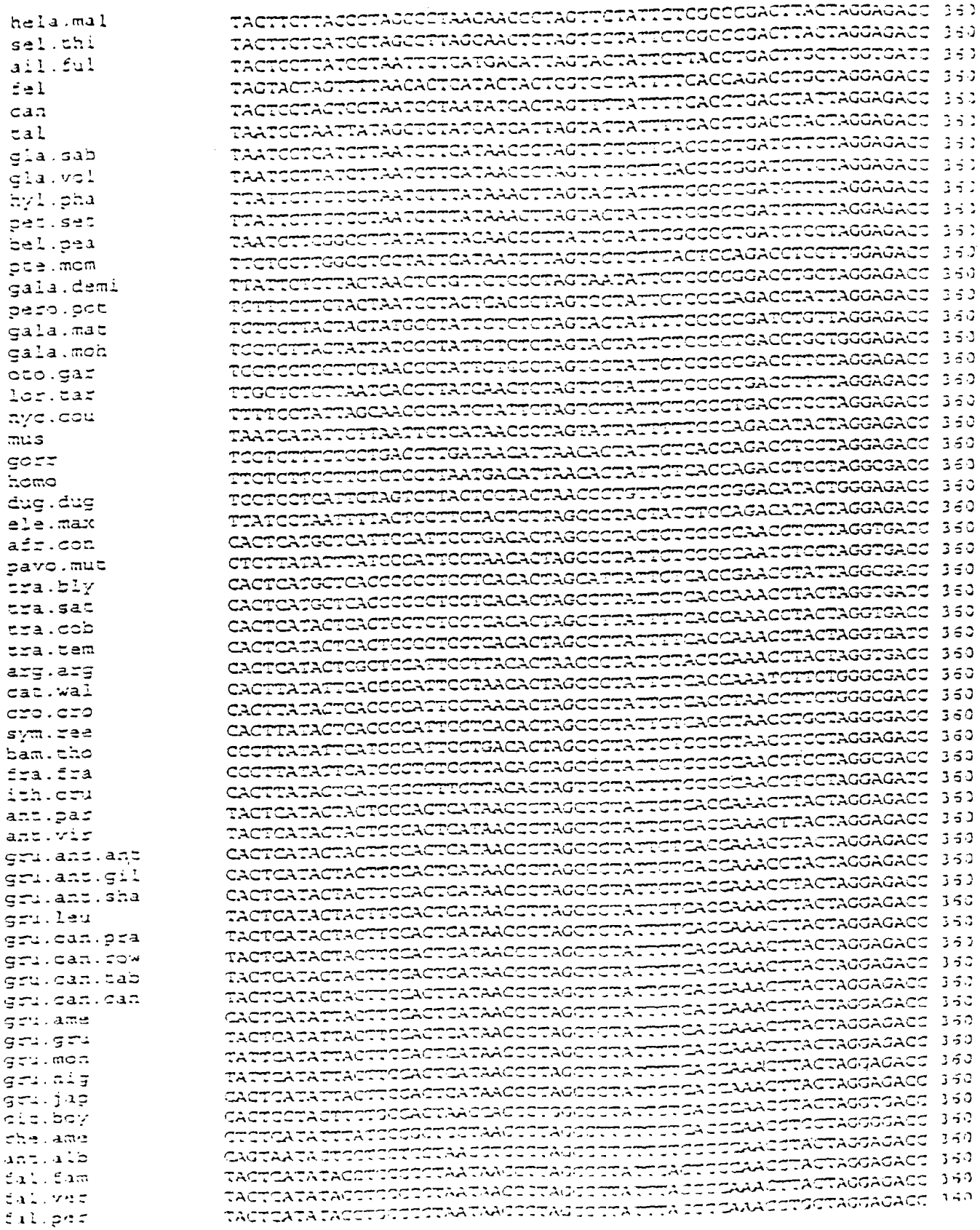
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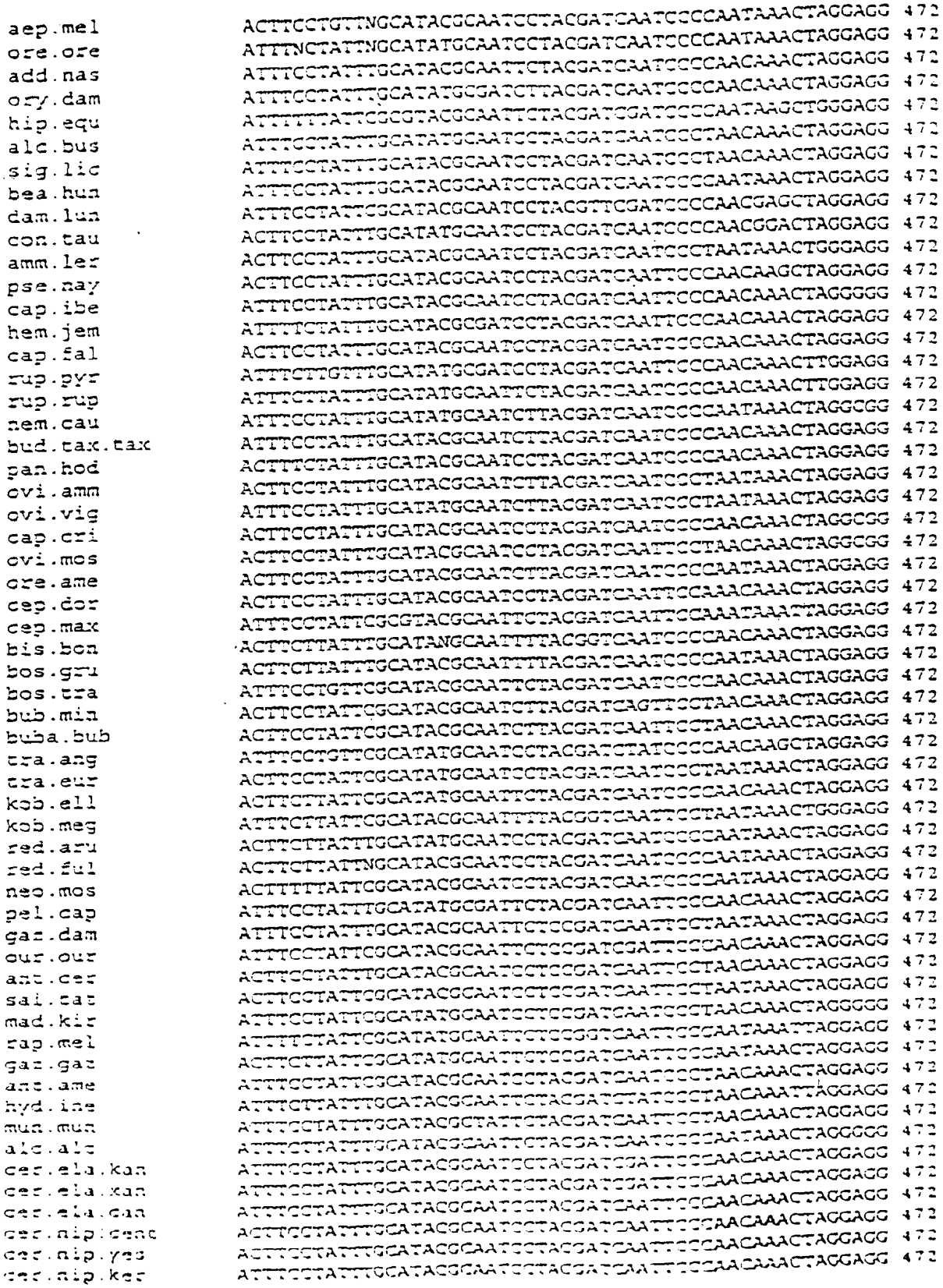
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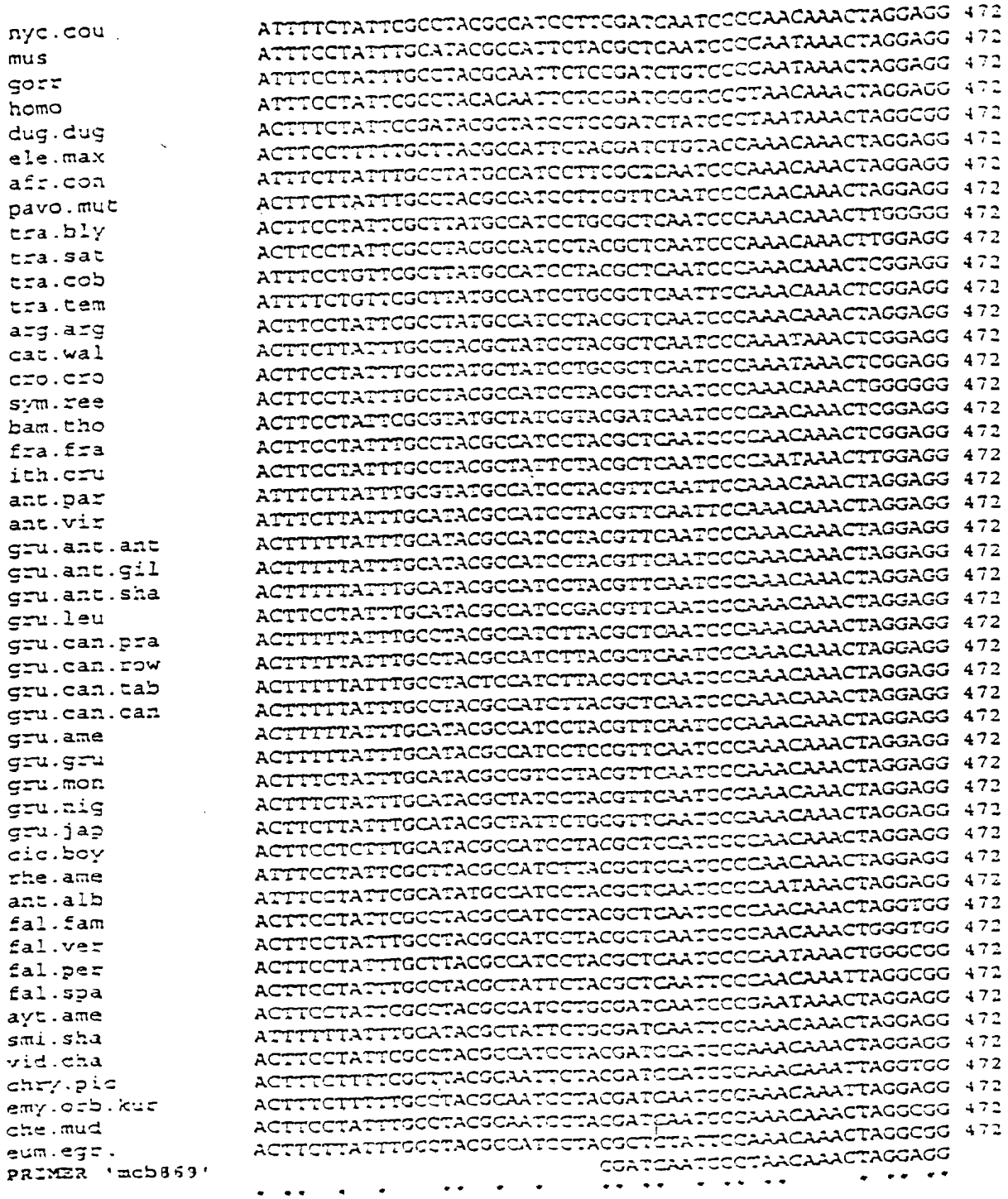
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Results for RID 984593689-1224-27770

BLASTN 2.1.2 [Nov-13-2000]

Reference:
Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 984593689-1224-27770

Query=
(328 letters)

Database: Sequences from complete mitochondrial genomes
129 sequences; 3,164,247 total letters

If you have any problems or questions with the results of this search please refer to the BLAST FAQs

Taxonomy reports

Distribution of 80 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments

Score

Sequences producing significant alignments:

		(bits)	Value
ref|NC_001700.1|	Felis catus mitochondrion, complete genome	365	e-101
ref|NC_001325.1|	Phoca vitulina mitochondrion, complete genome	198	1e-51
ref|NC_002008.1|	Canis familiaris mitochondrion, complete g...	190	4e-49
ref|NC_001602.1|	Halichoerus grypus mitochondrion, complete...	180	3e-46
ref|NC_000884.1|	Cavia porcellus complete mitochondrial genome	176	5e-45
ref|NC_001808.1|	Ceratotherium simum mitochondrion, complet...	165	2e-41
ref|NC_001892.1|	Myoxus glis mitochondrion, complete genome	153	8e-38
ref|NC_001788.1|	Equus asinus mitochondrion, complete genome	151	3e-37
ref|NC_002078.1|	Orycteropus afer complete mitochondrial ge...	149	1e-36
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Alignments

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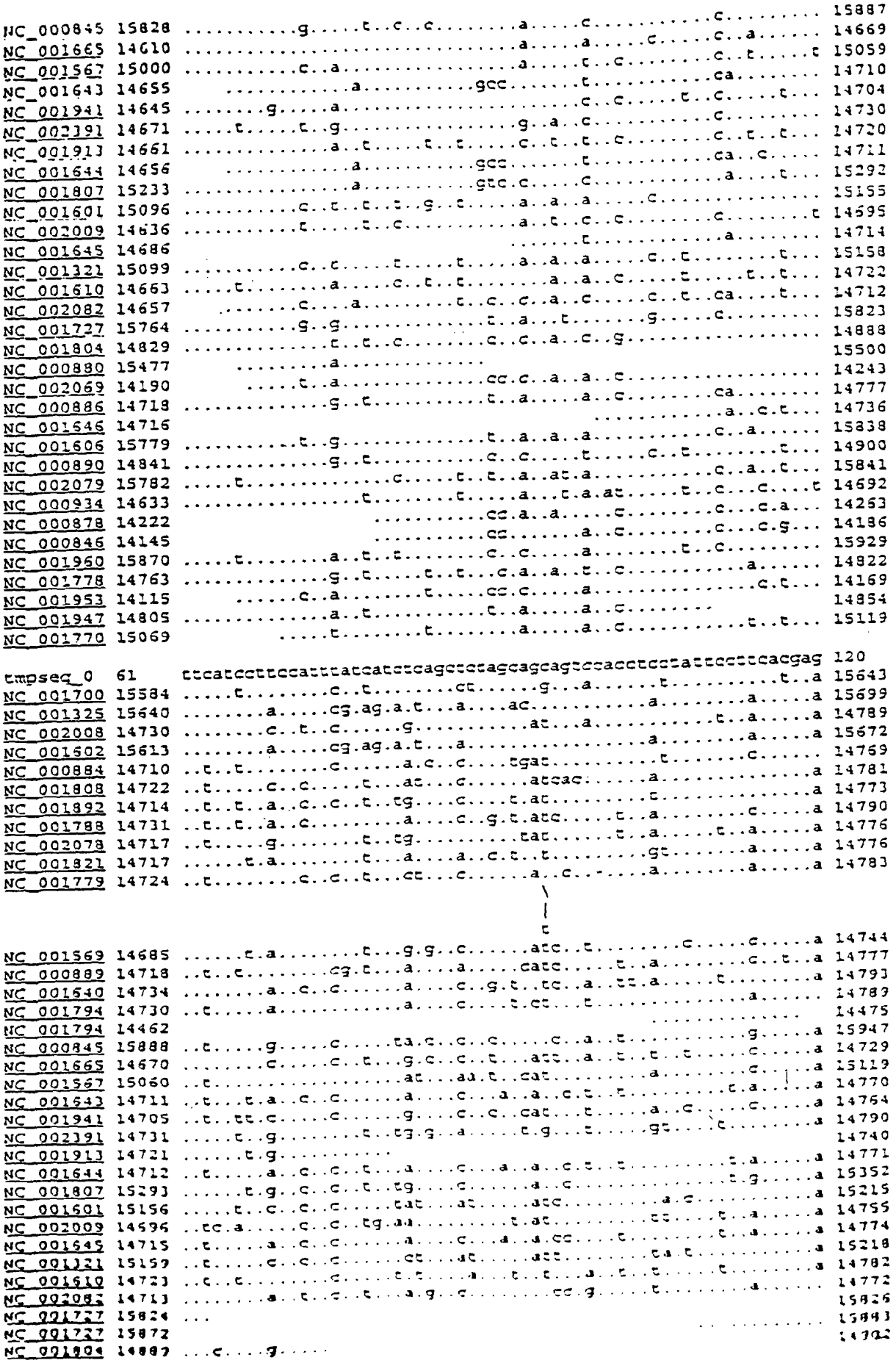

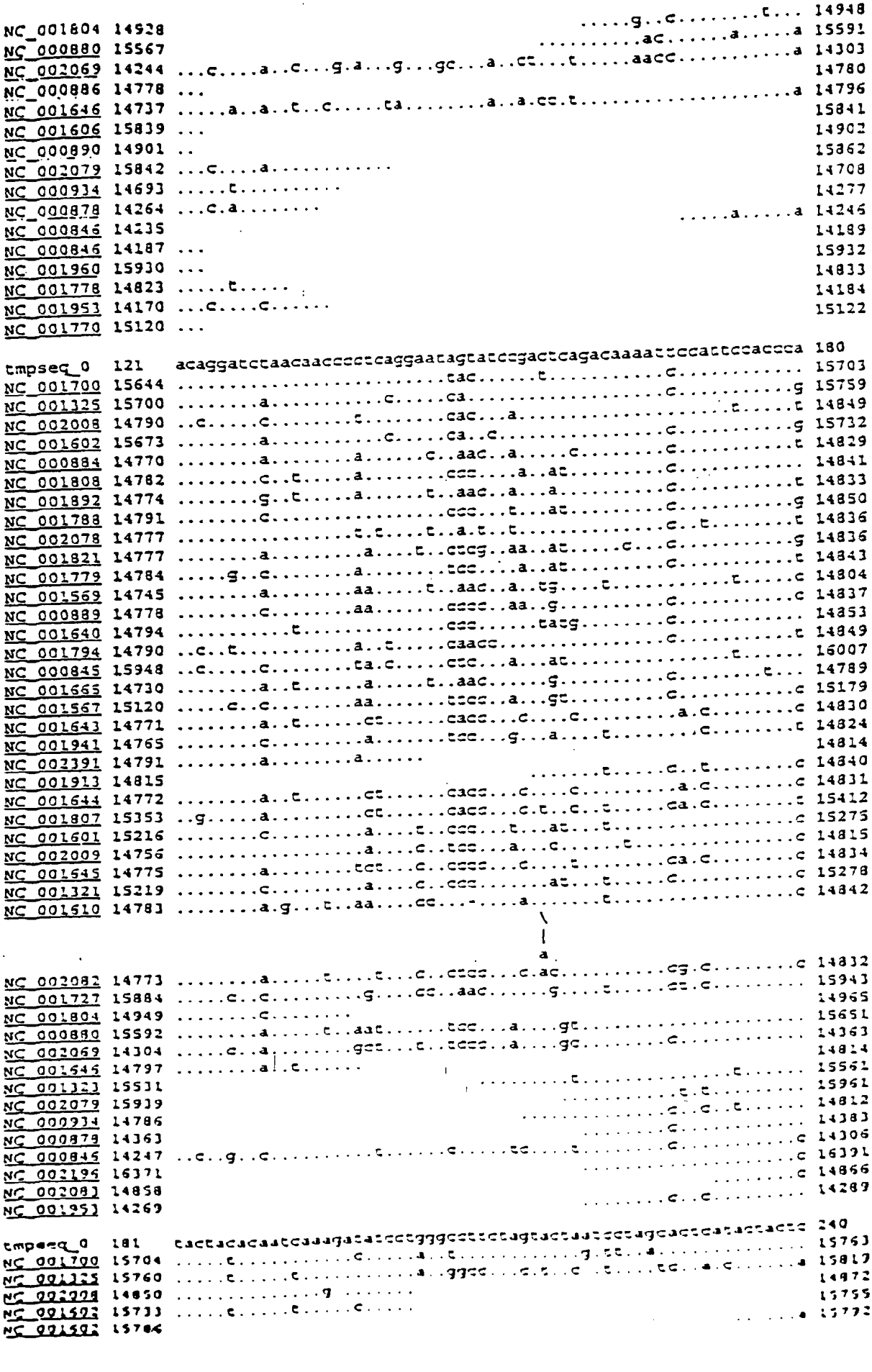

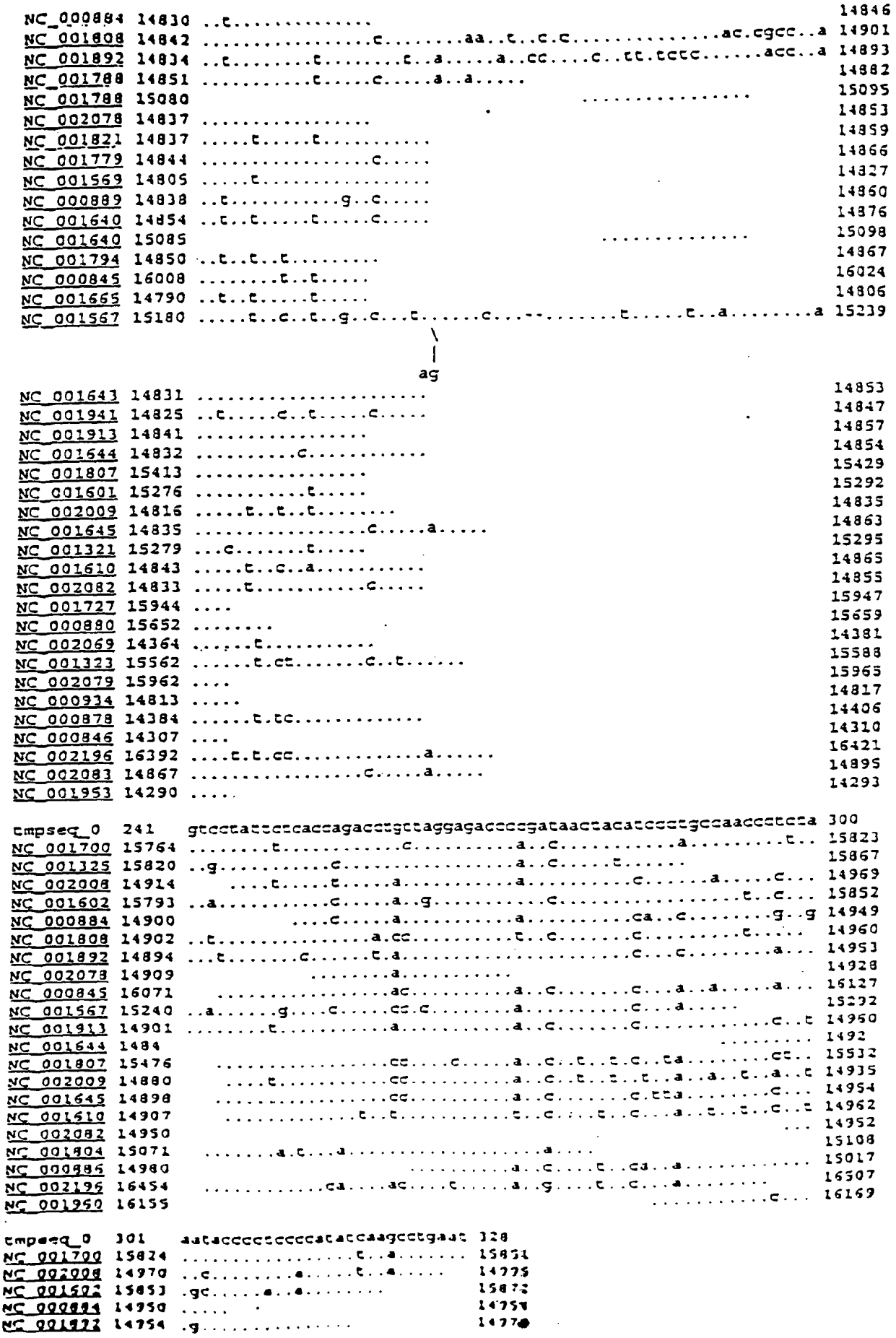
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NC_001808 14842 .....c.....aa..t..c.c.....ac.cgcc..a
NC_001892 14834 ..t.....t.....t..a.....a..cc....c..tt.tctc.....acc..a
NC_001788 14851 .....t.....c.....a..a.....
NC_001788 15080 .....
NC_002078 14837 .....
NC_001821 14837 .....t.....t.....
NC_001779 14844 .....c.....
NC_001569 14805 .....t.....
NC_000889 14838 ..t.....g..c.....
NC_001640 14854 ..t..t.....t.....c.....
NC_001640 15085 .....
NC_001794 14850 ..t..t..t.....
NC_000845 16008 .....t..t.....
NC_001665 14790 ..t..t.....t.....
NC_001567 15180 .....t..c..t..g..c...t.....c.....t.....t..a.....a
ag
NC_001643 14831 .....
NC_001941 14825 ..t.....c..t.....c.....
NC_001913 14841 .....
NC_001644 14832 .....c.....
NC_001807 15413 .....
NC_001601 15276 .....t.....
NC_002009 14816 .....t..t..t.....
NC_001645 14835 .....c.....a.....
NC_001321 15279 ...c.....t.....
NC_001610 14843 .....t..c..a.....
NC_002082 14833 .....t.....c.....
NC_001727 15944 ....
NC_000880 15652 .....
NC_002069 14364 .....t.....
NC_001323 15562 .....t.ct.....c..t.....
NC_002079 15962 ....
NC_000934 14813 .....
NC_000878 14384 .....t.tc.....
NC_000846 14307 ....
NC_002196 16392 ....t.t.cc.....a.....
NC_002083 14867 .....c.....a.....
NC_001953 14290 .....
tmpseq_0 241 gtcctattcccaccagaccctgttaggagaccccgataactacatcccctgccaaccctcta
NC_001700 15764 .....t.....c.....a..c.....a.....t..
NC_001325 15820 ..g.....c.....a..c.....t.....
NC_002008 14914 ....t.....t.....a.....a.....c.....a.....c...
NC_001602 15793 ..a.....c.....a..g.....c.....t..c...
NC_000884 14900 ....c.....a.....a.....ca..c.....g..g
NC_001808 14902 ..t.....a.cc.....t..c.....c.....t.....
NC_001892 14894 ...t.....c.....t.a.....c...c.....a...
NC_002078 14909 .....a.....
NC_000845 16071 .....ac.....a..c.....c...a..a.....a...
NC_001567 15240 ..a.....g....c.....cc.c.....a.....c...a.....
NC_001913 14901 .....t.....a.....a..c.....c.....c..t
NC_001644 1484 .....
NC_001807 15476 .....cc....c.....a..c..t..t.c..ta.....cc..
NC_002009 14880 ....t.....cc.....a..c..t..t..t..a..a..t..a..t
NC_001645 14898 .....cc.....a..c.....c.tta.....c...
NC_001610 14907 .....t..t.....t..c...t..c...a..t..t..c..t
NC_002082 14950 .....
NC_001804 15071 .....a.t...a.....a....
NC_000886 14980 .....a..c....t..ca..a.....
NC_002195 16454 .....ca....ac....t.....a..g....t..c...a.....
NC_001950 16155 .....c...
tmpseq_0 301 aatacccctccccatatcaagcctgaat 328
NC_001700 15824 .....t..a..... 15854
NC_002008 14970 ..c.....a.....t..a..... 14775
NC_001602 15853 .gc.....a..a..... 15872
NC_000884 14950 14754
NC_001323 14754 .g..... 14774

```
NC_001779 3081           .............    3094
NC_000845 16128 ..c.....a........        16144
NC_001911 14961 .....................    14980
NC_001644 1493  ...c.....                1501
NC_001807 15533 ..c...........c........c.... 15560
NC_002009 14936 ..................t.....a.... 14963
NC_001645 14955 .gc.....a.....c.....     14974
NC_001610 14963 ..c.....g..t...........a.... 14990
NC_002082 14953 ..c...........c.....     14972
NC_001960 16170 gt...t..a..t................ 16197
NC_001951 14426       .................c.... 14437
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Database: Sequences from complete mitochondrial genomes
Posted date: Jun 28, 2000 10:56 AM
Number of letters in database: 3,164,247
Number of sequences in database: 129

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1.37	0.711	1.31

Gapped Lambda	K	H
1.37	0.711	1.31

Matrix: blastn matrix:1 -3
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 788
Number of Sequences: 129
Number of extensions: 788
Number of successful extensions: 168
Number of sequences better than 10.0: 77
length of query: 328
length of database: 3,164,247
effective HSP length: 15
effective length of query: 313
effective length of database: 3,162,312
effective search space: 989803656
effective search space used: 989803656
T: 0
A: 30
X1: 6 (11.9 bits)
X2: 15 (29.7 bits)
S1: 12 (24.3 bits)
S2: 14 (28.2 bits)

Table 4

BLASTN 2.1.2 [Nov-13-2000]

Reference:
Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 984593400-28182-3122

Query=
(328 letters)

Database: nt
807,597 sequences; 2,863,827,885 total letters

If you have any problems or questions with the results of this search please refer to the BLAST FAQs

Taxonomy reports

Distribution of 50 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments

Sequences producing significant alignments:

		Score (bits)	E Value
gb|AY005809.1|	Panthera pardus cytochrome b gene, partial c...	603	e-170
gb|AF053054.1|AF053054	Panthera tigris sumatrae isolate Su1...	527	e-147
gb|AF053053.1|AF053053	Panthera tigris tigris isolate B7 mi...	527	e-147
gb|AF053050.1|AF053050	Panthera tigris corbetti isolate C2 ...	476	e-132
gb|AF053049.1|AF053049	Panthera tigris corbetti isolate C1 ...	476	e-132
gb|AF053025.1|AF053025	Panthera tigris tigris isolate B9 cy...	460	e-127
gb|AF053024.1|AF053024	Panthera tigris tigris isolate B8 cy...	460	e-127
gb|AF053023.1|AF053023	Panthera tigris tigris isolate B7 cy...	460	e-127
gb|AF053022.1|AF053022	Panthera tigris tigris isolate B6 cy...	460	e-127
gb|AF053021.1|AF053021	Panthera tigris tigris isolate B5 cy...	460	e-127
gb|AF053018.1|AF053018	Panthera tigris tigris isolate B2 cy...	460	e-127
gb|AF053051.1|AF053051	Panthera tigris corbetti isolate C3 ...	452	e-125
gb|AF053048.1|AF053048	Panthera tigris sumatrae isolate Su1...	452	e-125
gb|AF053047.1|AF053047	Panthera tigris sumatrae isolate Su9...	452	e-125
gb|AF053046.1|AF053046	Panthera tigris sumatrae isolate Su7...	452	e-125
gb|AF053045.1|AF053045	Panthera tigris sumatrae isolate Su6...	452	e-125
gb|AF053044.1|AF053044	Panthera tigris sumatrae isolate Su5...	452	e-125
gb|AF053042.1|AF053042	Panthera tigris sumatrae isolate Su3...	452	e-125
gb|AF053041.1|AF053041	Panthera tigris sumatrae isolate Su2...	452	e-125
gb|AF053040.1|AF053040	Panthera tigris sumatrae isolate Su1...	452	e-125
gb|AF053039.1|AF053039	Panthera tigris altaica isolate S15 ...	452	e-125
gb|AF053038.1|AF053038	Panthera tigris altaica isolate S14 ...	452	e-125
gb|AF053037.1|AF053037	Panthera tigris altaica isolate S13 ...	452	e-125
gb|AF053036.1|AF053036	Panthera tigris altaica isolate S12 ...	452	e-125
gb|AF053035.1|AF053035	Panthera tigris altaica isolate S11 ...	452	e-125
gb|AF053034.1|AF053034	Panthera tigris altaica isolate S10 ...	452	e-125
gb|AF053033.1|AF053033	Panthera tigris altaica isolate S8 c...	452	e-125
gb|AF053032.1|AF053032	Panthera tigris altaica isolate S7 c...	452	e-125
gb|AF053031.1|AF053031	Panthera tigris altaica isolate S6 c...	452	e-125
gb|AF053030.1|AF053030	Panthera tigris altaica isolate S5 c...	452	e-125
gb|AF053029.1|AF053029	Panthera tigris altaica isolate S4 c...	452	e-125
gb|AF053028.1|AF053028	Panthera tigris altaica isolate S3 c...	452	e-125
gb|AF053027.1|AF053027	Panthera tigris altaica isolate S2 c...	452	e-125
gb|AF053026.1|AF053026	Panthera tigris altaica isolate S1 c...	452	e-125
gb|AF053020.1|AF053020	Panthera tigris tigris isolate B4 cy...	452	e-125
gb|AF053019.1|AF053019	Panthera tigris tigris isolate B3 cy...	444	e-122
gb|AF053043.1|AF053043	Panthera tigris sumatrae isolate Su4...	444	e-122
emb|X82301.1|MIPTCYTB	P.tigris mitochondrial cytochrome b gene	440	e-121
gb|AF053052.1|AF053052	Panthera leo cytochrome b (cytb) gen...	438	e-121
emb|X82300.1|MIPLCYTBG	P.leo mitochondrial cytochrome b gene	399	e-106
dbj|AB004238.1|AB004238	Felis catus mitochondrial DNA for c...	381	e-103
dbj|AB004237.1|AB004237	Felis catus mitochondrial DNA for c...	377	e-102
emb|X82296.1|MIFDCYTB	F.domesticus mitochondrial cytochrome...	365	1e-98
ref|NC_001700.1|	Felis catus mitochondrion, complete genome	365	1e-98
gb|U20753.1|FCU20753	Felis catus mitochondrion, complete ge...	276	7e-72
gb|AF125145.1|AF125145	Viverricula indica cytochrome b gene...	270	4e-70
gb|AF125144.1|AF125144	Chrotogale owstoni cytochrome b gene...	256	7e-66
gb|AF154975.1|AF154975	Martes martes specimen_voucher AF175...	256	7e-66
dbj|AB051237.1|AB051237	Martes martes mitochondrial cytb ge...	246	6e-63
gb|AF125149.1|AF125149	Viverra tangalunga cytochrome b gene...		

Alignments

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                 ..........g..........................t.......................... 98
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AF053053   487   ..........g..........................c.......................... 546
AF053050   487   ..........g..t.......................c.......................... 546
AF053049   487   ..........g..t.......................c.......................... 546
AF053025   487   ..........g..t.......................c.......................... 546
AF053024   487   ..........g..t.......................c.......................... 546
AF053023   487   ..........g..t.......................c.......................... 546
AF053022   487   ..........g..t.......................c.......................... 546
AF053021   487   ..........g..t.......................c.......................... 546
AF053018   487   ..........g..t.......................c.......................... 546
AF053051   487   ..........g..t.......................c.......................... 546
AF053048   487   ..........g..t.......................c.......................... 546
AF053047   487   ..........g..t.......................c.......................... 546
AF053046   487   ..........g..t.......................c.......................... 546
AF053045   487   ..........g..t.......................c.......................... 546
AF053044   487   ..........g..t.......................c.......................... 546
AF053042   487   ..........g..t.......................c.......................... 546
AF053041   487   ..........g..t.......................c.......................... 546
AF053040   487   ..........g..t.......................c.......................... 546
AF053039   487   ..........g..t.......................c.......................... 546
AF053038   487   ..........g..t.......................c.......................... 546
AF053037   487   ..........g..t.......................c.......................... 546
AF053036   487   ..........g..t.......................c.......................... 546
AF053035   487   ..........g..t.......................c.......................... 546
AF053034   487   ..........g..t.......................c.......................... 546
AF053033   487   ..........g..t.......................c.......................... 546
AF053032   487   ..........g..t.......................c.......................... 546
AF053031   487   ..........g..t.......................c.......................... 546
AF053030   487   ..........g..t.......................c.......................... 546
AF053029   487   ..........g..t.......................c.......................... 546
AF053028   487   ..........g..t.......................c.......................... 546
AF053027   487   ..........g..t.......................c.......................... 546
AF053026   487   ..........g..t.......................c.......................... 546
AF053020   487   ..........g..t.......................c.......................... 546
AF053019   487   ..........g..t.......................c.......................... 546
AF053043   487   ..........g..t.......................c.......................... 546
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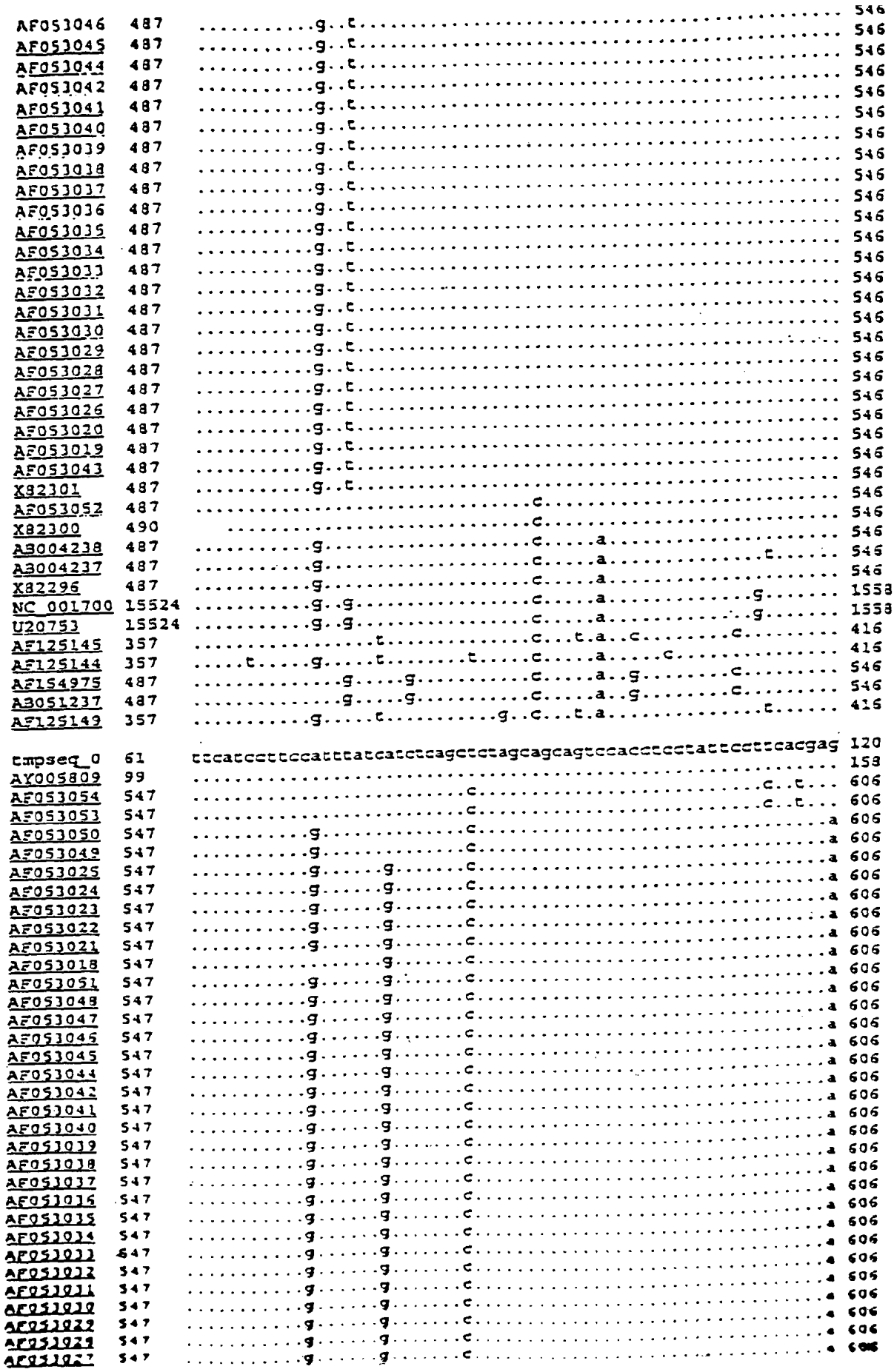

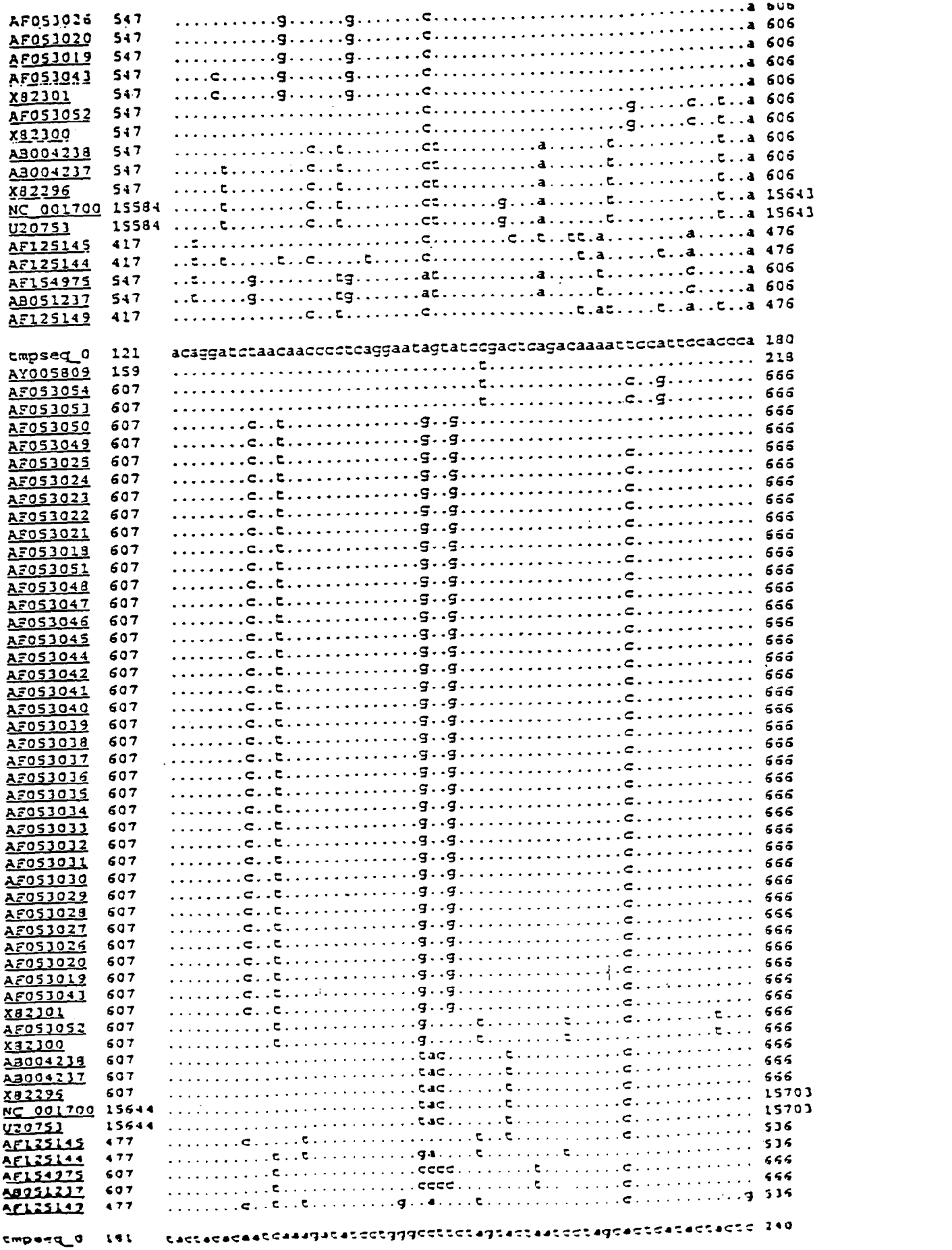

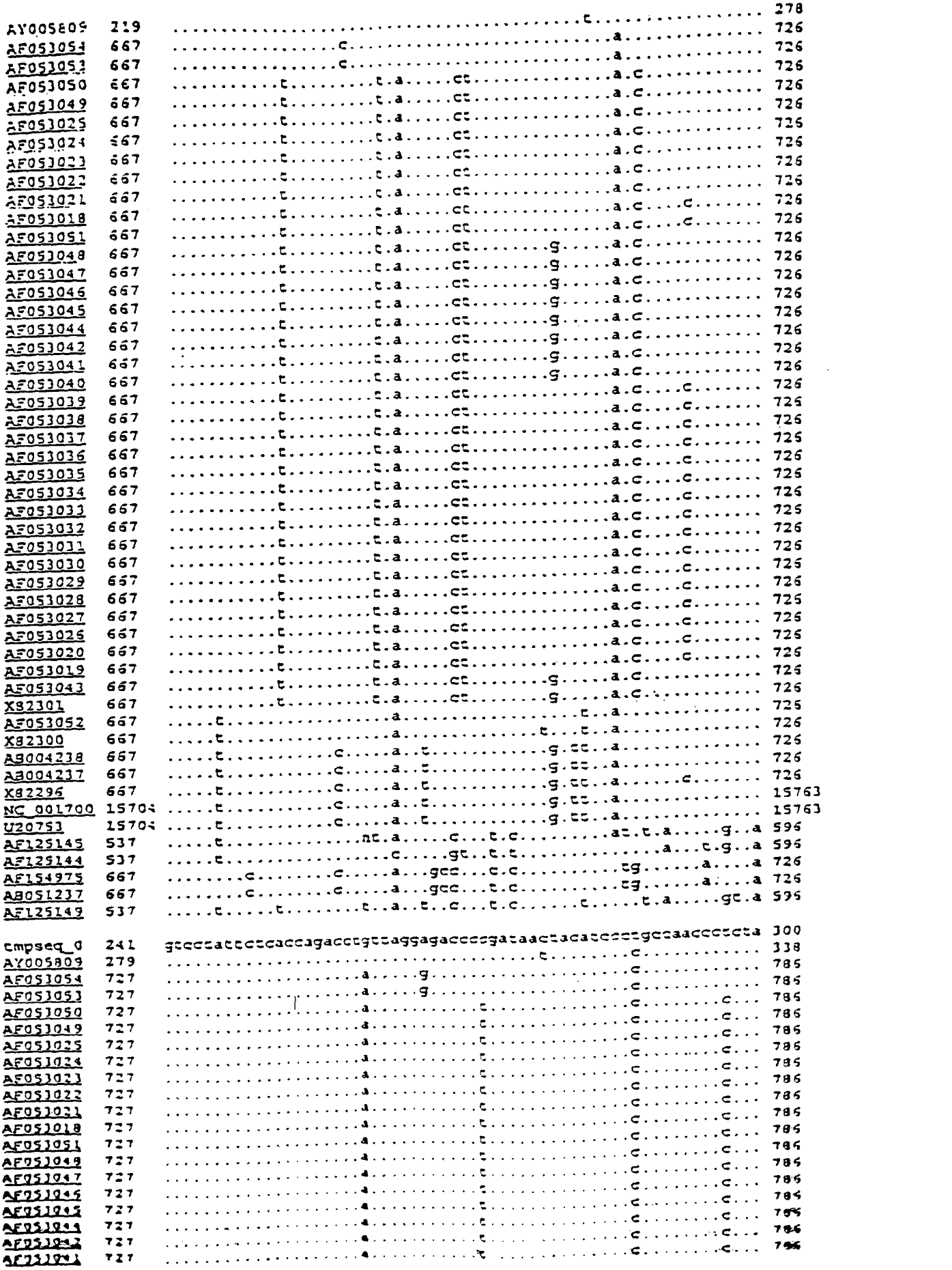

```
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AF053039  727  .....a.....t.....c.....c...  786
AF053038  727  .....a.....t.....c.....c...  786
AF053037  727  .....a.....t.....c.....c...  786
AF053036  727  .....a.....t.....c.....c...  786
AF053035  727  .....a.....t.....c.....c...  786
AF053034  727  .....a.....t.....c.....c...  786
AF053033  727  .....a.....t.....c.....c...  786
AF053032  727  .....a.....t.....c.....c...  786
AF053031  727  .....a.....t.....c.....c...  786
AF053030  727  .....a.....t.....c.....c...  786
AF053029  727  .....a.....t.....c.....c...  786
AF053028  727  .....a.....t.....c.....c...  786
AF053027  727  .....a.....t.....c.....c...  786
AF053026  727  .....a.....t.....c.....c...  786
AF053020  727  .....a.....t.....c.....c...  786
AF053019  727  .....a.....t.....c.....c...  786
AF053043  727  .....a.....t.....c.....c...  786
X82301    727  .....a.....t.....c.....c...  786
AF053052  727  .....a.....t.....c.....t.c...c.....t.....  786
X82300    727  .....a.....t.....c.....t.c...c.....t.....  786
AB004238  727  .....t.....c.....a..c.g.....a.....t..  786
AB004237  727  .....t.....c.....a..c.....a.....t..  786
X82296    727  .....r..t.....c.....a..c.....a.....t..  786
NC_001700 15764 .....t.....c.....a..c.....a.....t..  15823
U20753    15764 .....t.....c.....a..c.....a.....t..  15823
AF125145  597  .....t.....t.....a.....t.....t..c.....  650
AF125144  597  ..t.....t.....t.....t.....a..c.....c.....a.....  656
AF154975  727  ..a.....c.....c.g.....a..c.....c.....a..c  786
AB051237  727  ..a.....c.....c.g.....a..c.....c.....a..c  786
AF125149  597  .....t.....cc.....a.....t.c.....  656

tmpseq_0  301  aataccccctccccatatcaagcctgaat  328
AY005809  339  .....  366
AF053054  787  ..c.....  808
AF053053  787  ..c.....  808
AF053050  787  .....t.....c....  814
AF053049  787  .....t.....c....  814
AF053025  787  .....t.....c....  814
AF053024  787  .....t.....c....  814
AF053023  787  .....t.....c....  814
AF053022  787  .....t.....c....  814
AF053021  787  .....t.....c....  814
AF053018  787  .....t.....c....  814
AF053051  787  .....t.....c....  814
AF053048  787  .....t.....c....  814
AF053047  787  .....t.....c....  814
AF053046  787  .....t.....c....  814
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AF053029  787  .....t.....c....  814
AF053028  787  .....t.....c....  814
AF053027  787  .....t.....c....  814
AF053026  787  .....t.....c....  814
AF053020  787  .....t.....c....  814
AF053019  787  .....t.....c....  814
AF053043  787  .....t.....c....  814
X82301    787  .....t.....c....  814
```

```
AF053052  787   .gc.................a.....  812
X82200    787   .gc.................a.....  814
AB004238  787   ..................t..a.....  814
AB004237  787   ..................t..a.....  814
X82296    787   ..................t..a.....  814
NC_001700 15824 ..................t..a..... 15851
U20753    15824 ..................t..a..... 15851
AF125144  657   ..c.....                     664
AF154975  787   ..c..a..a........            803
AB051237  787   ..c..a..a........            803
AF125149  657   ..c.....                     664
```

Database: nt
Posted date: Mar 2, 2001 12:20 AM
Number of letters in database: 2,863,827,885
Number of sequences in database: 807,597

Lambda	K	H
1.37	0.711	1.31

Gapped

Lambda	K	H
1.37	0.711	1.31

Matrix: blastn matrix:1 -3
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 460542
Number of Sequences: 807597
Number of extensions: 460542
Number of successful extensions: 22671
Number of sequences better than 10.0: 6487
length of query: 328
length of database: 2,863,827,885
effective HSP length: 20
effective length of query: 308
effective length of database: 2,847,675,945
effective search space: 877084191060
effective search space used: 877084191060
T: 0
A: 30
X1: 6 (11.9 bits)
X2: 15 (29.7 bits)
S1: 12 (24.3 bits)
S2: 19 (38.2 bits)

Table 5. Reference animals and the allocated code numbers included in the study

SN.	Code number	Name of the animal	Zoological name
1	bhz25t	Indian tiger	*Panthera tigris tigris*
2	bhz26t	Indian tiger	*Panthera tigris tigris*
3	bhz30t	Indian tiger	*Panthera tigris tigris*
4	bhz45t	Indian tiger	*Panthera tigris tigris*
5	bhz56t	Indian tiger	*Panthera tigris tigris*
6	bhz63t	Indian tiger	*Panthera tigris tigris*
7	bhz20wt	Indian white tiger	*Panthera tigris bengalensis*
8	bhz22wt	Indian white tiger	*Panthera tigris bengalensis*
9	bhz23wt	Indian white tiger	*Panthera tigris bengalensis*
10	bhz28wt	Indian white tiger	*Panthera tigris bengalensis*
11	gz1l	Normal leopard	*Panthera pardus*
12	gz2l	Normal leopard	*Panthera pardus*
13	gz3l	Normal leopard	*Panthera pardus*
14	gz21cl	Clouded leopard	*Neofelis nebulosa*
15	gz22cl	Clouded leopard	*Neofelis nebulosa*
16	darz14sl	Snow leopard	*Panthera unicia*
17	darz15sl	Snow leopard	*Panthera unicia*
18	darz16sl	Snow leopard	*Panthera unicia*
19	sbz22al	Asiatic lion	*Panthera leo persica*
20	sbz38al	Asiatic lion	*Panthera leo persica*
21	sbz39al	Asiatic lion	*Panthera leo persica*
22	humsk	Human	*Homo sapiens sapiens*
23	chimss	Chimpanzee	*Pan sp.*

Table 6. Multiple sequence alignments of the cytochrome b sequences of reference animals with the sequence obtained from confiscated animal remain

```
sbz22al          TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC 60
sbz38al          TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC 60
sbz39al          TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC 60
adil.flesh       TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCTACCCTGACACGATTCTTTGCCTTCCAC 60
gz1nl            TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCTACCTTGACACGATTCTTTGCCTTCCAC 60
gz2nl            TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCTACCTTGACACGATTCTTTGCCTTCCAC 60
gz3nl            TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCTACCTTGACACGATTCTTTGCCTTCCAC 60
bhz23wt          TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC 60
bhz28wt          TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC 60
bhz22wt          TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC 60
bhz20wt          TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC 60
bhz63t           TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC 60
bhz56t           TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC 60
bhz26t           TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC 60
bhz30t           TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC 60
bhz45t           TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC 60
bhz25t           TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC 60
dz14s1           TGAATCTGAGGAGGCTTCTCAGTACACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC 60
dz15s1           TGAATCTGAGGAGGCTTCTCAGTACACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC 60
dz16s1           TGAATCTGAGGAGGCTTCTCAGTACACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC 60
gz21c1           TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTTTTCGCCTTCCAC 60
gz22c1           TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTTTTCGCCTTCCAC 60
chimss           TGAATCTGAGGAGGCTACTCAGTAGACAGCCCTACCCTTACACGATTCTTCACCTTCCAC 60
humsk            TGAATCTGAGGAGGCTACTCAGTAGACAGTCCCACCCTCACACGATTCTTTACCTTTCAC 60
                 ********************* ******* ***    * *** * ******** **  **** ***

sbz22al          TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTGTTCCTCCATGAA 120
sbz38al          TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTGTTCCTCCATGAA 120
sbz39al          TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTGTTCCTCCATGAA 120
adil.flesh       TTCATCCTTCCATTTATCATCTCAGCTCTAGCAGCAGTCCACCTCCTATTCCTTCACGAG 120
gz1nl            TTCATCCTTCCATTTATCATCTCAGCTCTAGCAGCAGTCCACCTCCTATTCCTTCACGAG 120
gz2nl            TTCATCCTTCCATTTATCATCTCAGCTCTAGCAGCAGTCCACCTCCTATTCCTTCACGAG 120
gz3nl            TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCTCCATGAG 120
bhz23wt          TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCTCCATGAG 120
bhz28wt          TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCTCCATGAG 120
bhz22wt          TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCTCCATGAG 120
bhz20wt          TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCTCCATGAG 120
bhz63t           TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCTCCATGAG 120
bhz56t           TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCTCCATGAG 120
bhz26t           TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCTCCATGAG 120
bhz30t           TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCTCCATGAG 120
bhz45t           TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCTCCATGAG 120
bhz25t           TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCTCCATGAG 120
dz14s1           TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCTCCATGAG 120
dz15s1           TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCTCCATGAG 120
dz16s1           TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCTCCATGAG 120
gz21c1           TTCATCCTCCCATTTATCATCTCAGCCTTAGCAGCAGTTCACCTTCTATTTCTCCATGAA 120
gz22c1           TTCATCCTCCCATTTATCATCTCAGCCTTAGCAGCAGTTCACCTTCTATTTCTCCATGAA 120
chimss           TTTATCTTACCCTTCATTATCACAGCCCTAACAACACTTCATCTCCTATTCTTACACGAA 120
humsk            TTCATCTTGCCCTTCATTATTGCAGCCCTAGCAGCACTCCACCTCCTATTCTTGCACGAA 120
                 ** *** * ** ** ** ** ** **** ** ** ** * ** ** ** ** ** * ** **

sbz22al          ACAGGATCTAATAACCCCTCAGGAATGGTATCTGACTCAGATAAAATTCCATTCCATCCA 180
sbz38al          ACAGGATCTAATAACCCCTCAGGAATGGTATCTGACTCAGATAAAATTCCATTCCATCCA 180
```

```
sbz39a1         ACAGGATCTAATAACCCCTCAGGAATGGTATCTGACTCAGATAAAATTCCATTCCATCCA 180
adil.flesh      ACAGGATCTAACAACCCCTCAGGAATAGTATCCGACTCAGACAAAATTCCATTCCACCCA 180
gz1n1           ACAGGATCTAACAACCCCTCAGGAATAGTATCCGACTCAGACAAAATTCCATTCCACCCA 180
gz2n1           ACAGGATCTAACAACCCCTCAGGAATAGTATCTGACTCAGACAAAATTCCATTCCACCCA 180
gz3n1           ACAGGATCTAACAACCCCTCAGGAATAGTATCTGACTCAGACAAAATTCCATTCCACCCA 180
bhz23wt         ACAGGATCTAACAACCCCTCAGGAATAGTATCTGACTCAGACAAAATCCCGTTCCACCCA 180
bhz28wt         ACAGGATCTAACAACCCCTCAGGAATAGTATCTGACTCAGACAAAATCCCGTTCCACCCA 180
bhz22wt         ACAGGATCTAACAACCCCTCAGGAATAGTATCTGACTCAGACAAAATCCCGTTCCACCCA 180
bhz20wt         ACAGGATCTAACAACCCCTCAGGAATAGTATCTGACTCAGACAAAATCCCGTTCCACCCA 180
bhz63t          ACAGGATCTAACAACCCCTCAGGAATAGTATCTGACTCAGACAAAATCCCGTTCCACCCA 180
bhz56t          ACAGGATCTAACAACCCCTCAGGAATAGTATCTGACTCAGACAAAATCCCGTTCCACCCA 180
bhz26t          ACAGGATCTAACAACCCCTCAGGAATAGTATCTGACTCAGACAAAATCCCGTTCCACCCA 180
bhz30t          ACAGGATCTAACAACCCCTCAGGAATAGTATCTGACTCAGACAAAATCCCGTTCCACCCA 180
bhz45t          ACAGGATCTAACAACCCCTCAGGAATAGTATCTGACTCAGACAAAATCCCGTTCCACCCA 180
bhz25t          ACAGGATCTAACAACCCCTCAGGAATAGTATCTGACTCAGACAAAATCCCGTTCCACCCA 180
dz14s1          ACAGGATCTAACAACCCCTCAGGAATAGTATCTGACTCAGACAAAATCCCGTTCCACCCA 180
dz15s1          ACAGGATCTAACAACCCCTCAGGAATAGTATCTGACTCAGACAAAATCCCGTTCCACCCA 180
dz16s1          ACAGGATCTAACAACCCCTCAGGAATAGTATCTGACTCAGACAAAATCCCGTTCCACCCA 180
gz21c1          ACAGGATCCAATAACCCCTCAGGAATGGTATCCGATTCAGACAAAATCCCGTTCCACCCG 180
gz22c1          ACAGGATCCAATAACCCCTCAGGAATGGTATCCGATTCAGACAAAATCCCGTTCCACCCG 180
chimss          ACAGGATCAAATAACCCCCTGGGAATCACCTCCCACTCCGACAAAATTACCTTCCACCCC 180
humsk           ACGGGATCAAACAACCCCCTAGGAATCACCTCCCATTCCGATAAAATCATCTTCCACCCT 180
                ** ***** ** ******   *****    **  * ** ** *****    ***** **

sbz22a1         TACTATACAATCAAAGATATCCTAGGCCTTCTAGTACTAATCTTAACACTCATACTACTC 240
sbz38a1         TACTATACAATCAAAGATATCCTAGGCCTTCTAGTACTAATCTTAACACTCATACTACTC 240
sbz39a1         TACTATACAATCAAAGATATCCTAGGCCTTCTAGTACTAATCTTAACACTCATACTACTC 240
adil.flesh      TACTACACAATCAAAGATATCCTGGGCCTTCTAGTACTAATCCTAGCACTCATACTACTC 240
gz1n1           TACTACACAATCAAAGATATCCTGGGCCTTCTAGTACTAATCCTAGCACTCATACTACTC 240
gz2n1           TACTACACAATCAAAGACATCCTGGGCCTTCTAGTACTAATCTTAGCACTCATACTACTC 240
gz3n1           TACTACACAATCAAAGACATCCTGGGCCTTCTAGTACTAATCTTAGCACTCATACTACTC 240
bhz23wt         TACTACACAATCAAAGACATCCTGGGCCTTCTAGTACTAATCCTAACACTCATACTACTC 240
bhz28wt         TACTACACAATCAAAGACATCCTGGGCCTTCTAGTACTAATCCTAACACTCATACTACTC 240
bhz22wt         TACTACACAATCAAAGACATCCTGGGCCTTCTAGTACTAATCCTAACACTCATACTACTC 240
bhz20wt         TACTACACAATCAAAGACATCCTGGGCCTTCTAGTACTAATCCTAACACTCATACTACTC 240
bhz63t          TACTACACAATCAAAGACATCCTGGGCCTTCTAGTACTAATCCTAACACTCATACTACTC 240
bhz56t          TACTACACAATCAAAGACATCCTGGGCCTTCTAGTACTAATCCTAACACTCATACTACTC 240
bhz26t          TACTACACAATCAAAGACATCCTGGGCCTTCTAGTACTAATCCTAACACTCATACTACTC 240
bhz30t          TACTACACAATCAAAGACATCCTGGGCCTTCTAGTACTAATCCTAACACTCATACTACTC 240
bhz45t          TACTACACAATCAAAGACATCCTGGGCCTTCTAGTACTAATCCTAACACTCATACTACTC 240
bhz25t          TACTACACAATCAAAGACATCCTGGGCCTTCTAGTACTAATCCTAACACTCATACTACTC 240
dz14s1          TACTACACAATCAAAGACATCCTGGGCCTTCTAGTACTAATCCTAACACTCATACTACTC 240
dz15s1          TACTACACAATCAAAGACATCCTGGGCCTTCTAGTACTAATCCTAACACTCATACTACTC 240
dz16s1          TACTACACAATCAAAGACATCCTGGGCCTTCTAGTACTAATCCTAACACTCATACTACTC 240
gz21c1          TACTATACAATCAAAGATATCCTAGGCCTCCTAGTTCTAATTCTAGCGCTCACACTACTT 240
gz22c1          TACTATACAATCAAAGATATCCTAGGCCTCCTAGTTCTAATTCTAGCGCTCACACTACTT 240
chimss          TACTACACAATCAAAGATATCCTTGGCTTATTCCTTTTCCTCCTTATCCTTAATGACATTA 240
humsk           TACTACACAATCAAAGACGCCCTCGGCTTACTTCTCTTCCTTCTCTCCTTAATGACATTA 240
                ***** **********   *** *** * * * * * * *  * *  * *

sbz22a1         GTCCTATTCTCACCAGACCTATTAGGAGATCCCGACAACTATACCCCCGCCAATCCTCTA 300
sbz38a1         GTCCTATTCTCACCAGACCTATTAGGAGATCCCGACAACTATACCCCCGCCAATCCTCTA 300
sbz39a1         GTCCTATTCTCACCAGACCTATTAGGAGATCCCGACAACTATACCCCCGCCAATCCTCTA 300
adil.flesh      GTCCTATTCTCACCAGACCTGTTAGGAGACCCCGATAACTACATCCCTGCCAACCCTCTA 300
gz1n1           GTCCTATTCTCACCAGACCTGTTAGGAGACCCCGATAACTACATCCCCGCCAACCCTCTA 300
gz2n1           GTCCTATTCTCACCAGACCTGTTGGGAGACCCCGATAACTACATCCCCGCCAACCCTCTA 300
gz3n1           GTCCTATTCTCACCAGACCTATTAGGGGACCCCGATAACTACATCCCCGCCAACCCTCTA 300
bhz23wt         GTCCTATTCTCACCAGACCTATTAGGGGACCCCGATAACTACATCCCCGCCAACCCTCTA 300
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bhz28wt     GTCCTATTCTCACCAGACCTATTAGGGGACCCCGATAACTACATCCCCGCCAACCCTCTA 300
bhz22wt     GTCCTATTCTCACCAGACCTATTAGGGGACCCCGATAACTACATCCCCGCCAACCCTCTA 300
bhz20wt     GTCCTATTCTCACCAGACCTATTAGGGGACCCCGATAACTACATCCCCGCCAACCCTCTA 300
bhz63t      GTCCTATTCTCACCAGACCTATTAGGGGACCCCGATAACTACATCCCCGCCAACCCTCTA 300
bhz56t      GTCCTATTCTCACCAGACCTATTAGGGGACCCCGATAACTACATCCCCGCCAACCCTCTA 300
bhz26t      GTCCTATTCTCACCAGACCTATTAGGGGACCCCGATAACTACATCCCCGCCAACCCTCTA 300
bhz30t      GTCCTATTCTCACCAGACCTATTAGGGGACCCCGATAACTACATCCCCGCCAACCCTCTA 300
bhz45t      GTCCTATTCTCACCAGACCTATTAGGGGACCCCGATAACTACATCCCCGCCAACCCTCTA 300
bhz25t      GTCCTATTCTCACCAGACCTATTAGGGGACCCCGATAACTACATCCCCGCCAACCCTCTA 300
dz14sl      GTCCTATTCTCACCAGACCTATTAGGGGACGCCGATAACTACATCCCCGCCAACCCTCTA 300
dz15sl      GTCCTATTCTCACCAGACCTATTAGGGGACGCCGATAACTACATCCCCGCCAACCCTCTA 300
dz16sl      GTCCTATTCTCACCAGACCTATTAGGGGACGCCGATAACTACATCCCCGCCAACCCTCTA 300
gz21cl      GTTCTATTCTCCCCAGACCTACTAGGAGACCCTGACAATTACACTCCCGCCAACCCTCTA 300
gz22cl      GTTCTATTCTCCCCAGACCTACTAGGAGACCCTGACAATTACACTCCCGCCAACCCTCTA 300
chimss      ACACTATTCTCACCAGACCTCCTGGGCGATCCAGACAACTATACCCTAGCTAACCCCCTA 300
humsk       ACACTATTCTCACCAGACCTCCTAGGCGACCCAGACAATTATACCCTAGCCAACCCCTTA 300
                ******** ********  * ** **  * ** ** ** *  *  ** ** **  **

sbz22al     AGCACCCCTCCCCATATCAAACCTGAAT 328
sbz38al     AGCACCCCTCCCCATATCAAACCTGAAT 328
sbz39al     AGCACCCCTCCCCATATCAAACCTGAAT 328
adil.flesh  AATACCCCTCCCCATATCAAGCCTGAAT 328
gz1nl       AATACCCCTCCCCATATCAAGCCTGAAT 328
gz2nl       AATACCCCTCCCCATATCAAGCCTGAAT 328
gz3nl       AATACCCCTCCCCATATCAAGCCTGAAT 328
bhz23wt     AACACCCCTCCCCATATCAAGCGCGAAT 328
bhz28wt     AACACCCCTCCCCATATCAAGCGCGAAT 328
bhz22wt     AACACCCCTCCCCATATCAAGCGCGAAT 328
bhz20wt     AACACCCCTCCCCATATCAAGCGCGAAT 328
bhz63t      AACACCCCTCCCCATATCAAGCGCGAAT 328
bhz56t      AACACCCCTCCCCATATCAAGCGCGAAT 328
bhz26t      AACACCCCTCCCCATATCAAGCGCGAAT 328
bhz30t      AACACCCCTCCCCATATCAAGCGCGAAT 328
bhz45t      AACACCCCTCCCCATATCAAGCGCGAAT 328
bhz25t      AACACCCCTCCCCATATCAAGCGCGAAT 328
dz14sl      AACACCCCTCCCCATATCAAGCCCGAAT 328
dz15sl      AACACCCCTCCCCATATCAAGCCCGAAT 328
dz16sl      AACACCCCTCCCCATATCAAGCCCGAAT 328
gz21cl      AATACCCCTCCCCATATCAAGCCTGAAT 328
gz22cl      AATACCCCTCCCCATATCAAGCCTGAAT 328
chimss      AACACCCCACCCCACATTAAACCCGAAT 328
humsk       AACACCCCTCCCCACATCAAGCCCGAAT 328
            *  ***** ***** ** ** *  ****
```

Table 7a

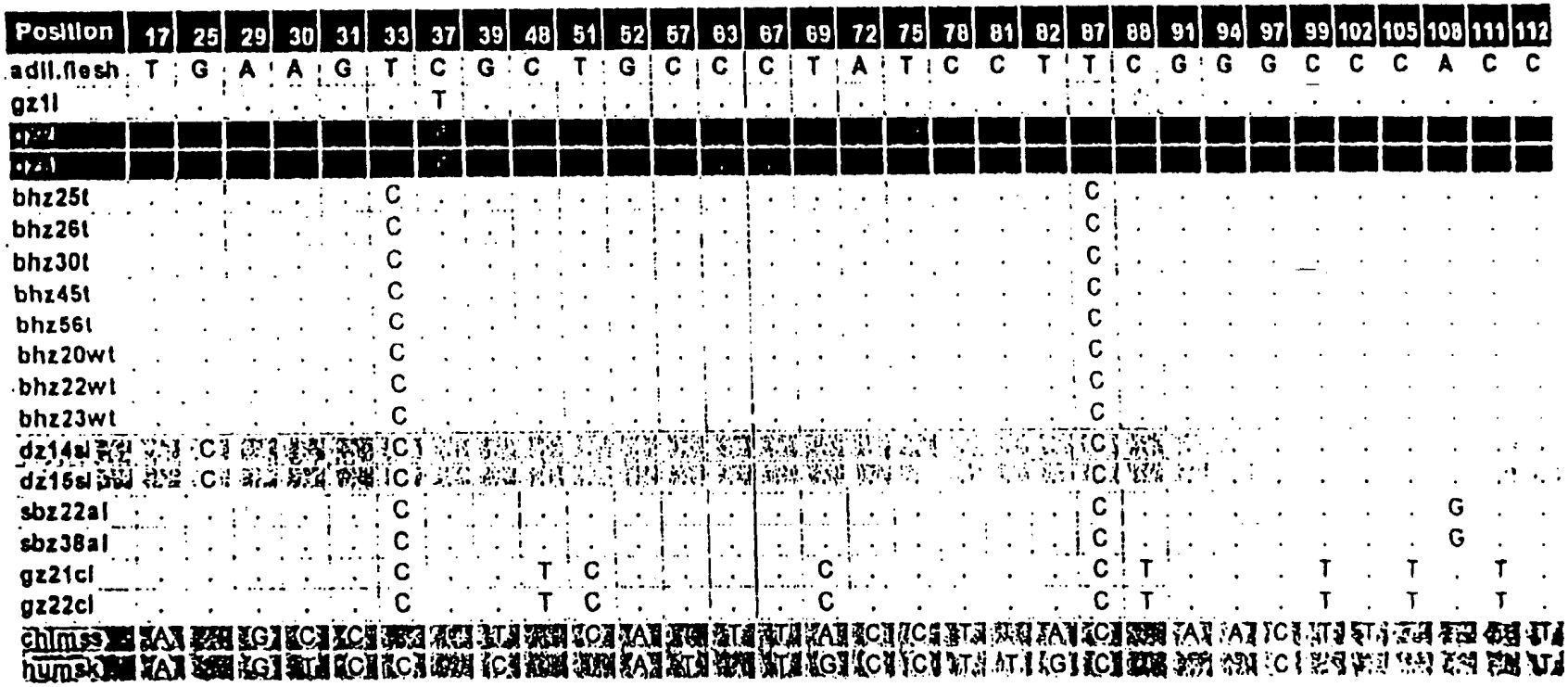
Position 17 25 29 30 31 33 37 39 48 51 52 57 63 67 69 72 75 78 81 82 87 88 91 94 97 99 102 105 108 111 112
adil.flesh T G A A G T C G C T G C C C T A T C C T T C G G G C C C A C C
gz1l . . . . . . T . . . .
bhz25t . . . . . C . . . . C . . . .
bhz26t . . . . . C . . . . C . . . .
bhz30t . . . . . C . . . . C . . . .
bhz45t . . . . . C . . . . C . . . .
bhz56t . . . . . C . . . . C . . . .
bhz20wt . . . . . C . . . . C . . . .
bhz22wt . . . . . C . . . . C . . . .
bhz23wt . . . . . C . . . . C . . . .
dz14al . C . . . C . . . . C . . . .
dz16al . C . . . C . . . . C . . . .
sbz22al . . . . . C . . . . C . . . . . G . . .
sbz38al . . . . . C . . . . C . . . . . G . . .
gz21cl . . . . . C . . T C . . . . . C . . . . . C T . . . T . T . T .
gz22cl . . . . . C . . T C . . . . . C . . . . . C T . . . T . T . T .
chimss A G C C C . . . . . A . . . . . C C . . . . A . C . . . . . .
humsk A G C C C . . . . . A . . . . G C C . . . . T . G . C . . . . .

Table 7b

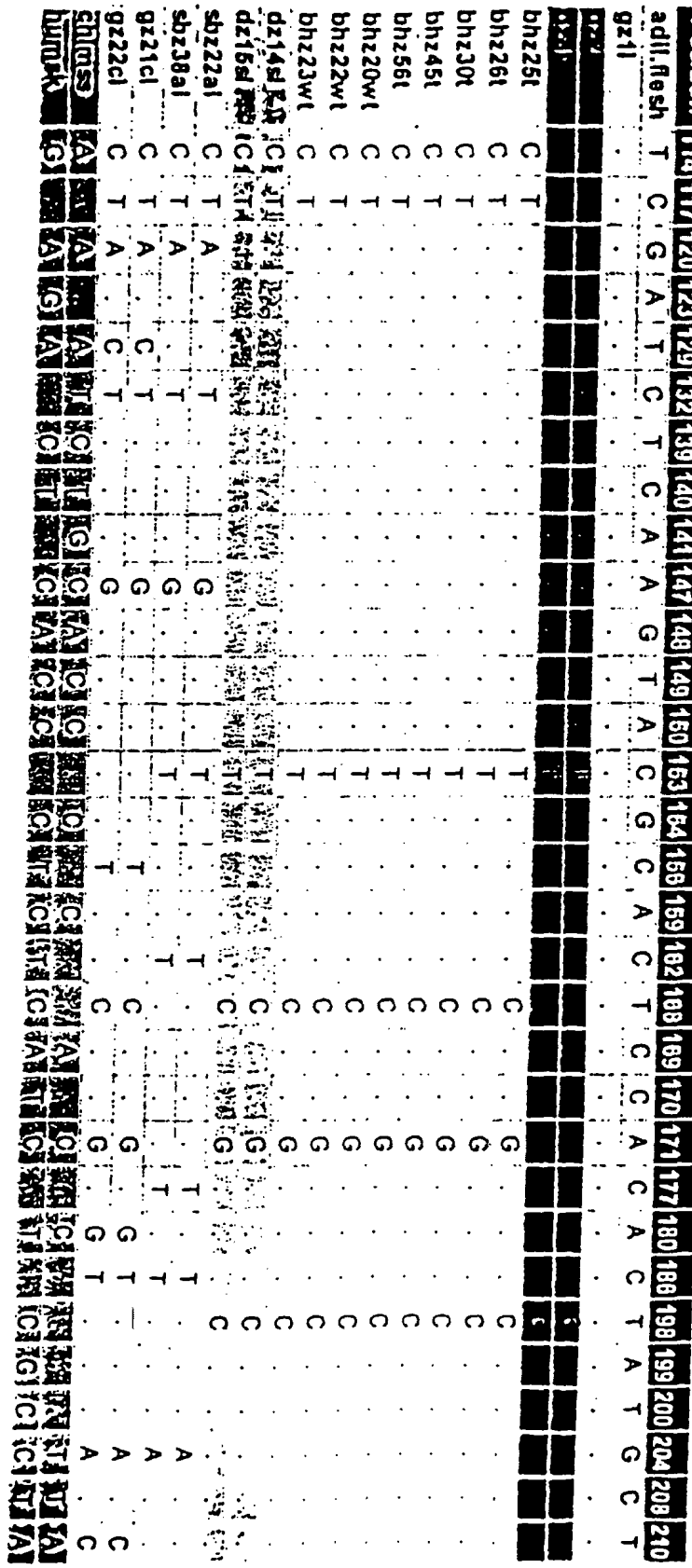

Table 7c

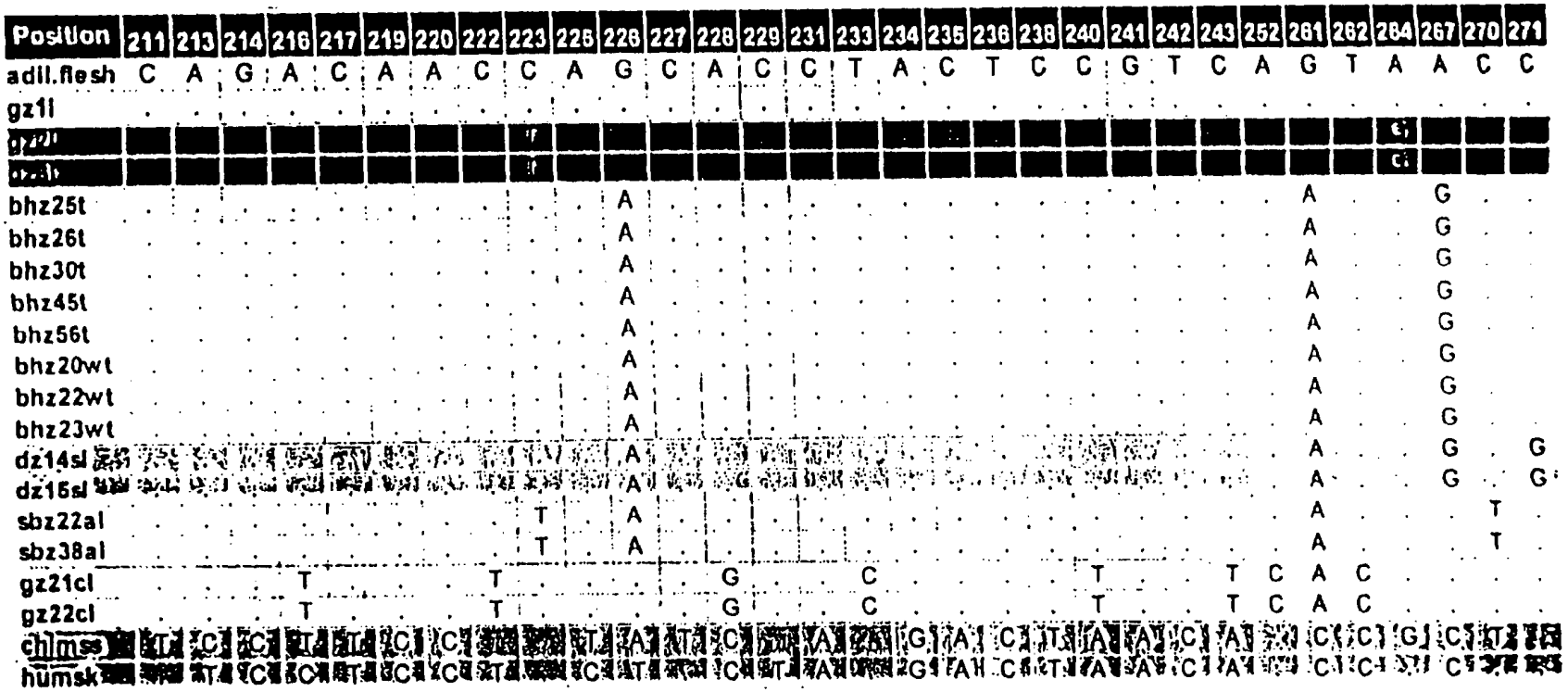
Position 211 213 214 216 217 219 220 222 223 225 226 227 228 229 231 233 234 235 236 238 240 241 242 243 252 261 262 264 267 270 271
adil.flesh C A G A C A A C C A G C A C C T A C T C C G T C A G T A A C C
gz1l
bhz25t
bhz26t
bhz30t
bhz45t
bhz56t
bhz20wt
bhz22wt
bhz23wt
dz14sl
dz15sl
sbz22al
sbz38al
gz21cl
gz22cl
chimsk
humsk

Table 7d

Position	273	276	279	282	284	285	287	288	291	294	297	298	302	303	309	315	318	321	323	324
adll.flesh	C	T	C	C	T	C	C	T	C	C	T	C	A	T	T	T	C	G	C	T
gz1l	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
[illegible]																				
[illegible]																				
bhz25t	.	.	.	.	.	.	.	C	.	.	.	.	.	C	.	.	.	.	G	C
bhz26t	.	.	.	.	.	.	.	C	.	.	.	.	.	C	.	.	.	.	G	C
bhz30t	.	.	.	.	.	.	.	C	.	.	.	.	.	C	.	.	.	.	G	C
bhz45t	.	.	.	.	.	.	.	C	.	.	.	.	.	C	.	.	.	.	G	C
bhz56t	.	.	.	.	.	.	.	C	.	.	.	.	.	C	.	.	.	.	G	C
bhz20wt	.	.	.	.	.	.	.	C	.	.	.	.	.	C	.	.	.	.	G	C
bhz22wt	.	.	.	.	.	.	.	C	.	.	.	.	.	C	.	.	.	.	G	C
bhz23wt	.	.	.	.	.	.	.	C	.	.	.	.	.	C	.	.	.	.	G	C
dz14sl	[illegible]							C						C					.	C
dz15sl	[illegible]							C						C					.	C
sbz22al	.	C	.	T	C	.	.	C	.	T	.	.	G	C	.	.	.	A	.	.
sbz38al	.	C	.	T	C	.	.	C	.	T	.	.	G	C	.	.	.	A	.	.
gz21cl	T	C	T	.	C	T	.	C	.	.	.	.	.	.	.	.	.	.	.	.
gz22cl	T	C	T	.	C	T	.	C	.	.	.	.	.	.	.	.	.	.	.	.
chimss	[illegible]																			
humsk	[illegible]																			

Table 8. Percent similarity matrix calculated by pair-vise comparisons of cytochrome b gene sequences revealed from 'adil.flesh' and different felids

	bhz20wt	bhz25t	dz14sl	humsk	chlmss	sbz22al	gz1L	gz2L	gz3L	gz21cl	adil.flesh
bhz20wt		100	99.1	81.7	78.7	93.3	95.1	95.4	95.4	89.6	95.4
bhz25t	100		99.1	81.7	78.7	93.3	95.1	95.4	95.4	89.6	95.4
dz14sl	99.1	99.1		81.4	78.4	93	94.8	95.1	95.1	89.3	95.1
humsk	81.7	81.7	81.4		86.9	79.6	81.1	80.2	80.2	79	81.4
chlmss	78.7	78.7	78.4	86.9		78.7	79.6	78.7	78.7	76.8	79.9
sbz22al	93.3	93.3	93	79.6	78.7		92.1	92.4	92.4	89	92.4
gz1L	95.1	95.1	94.8	81.1	79.6	92.1		98.5	98.5	89.3	99.7
gz2L	95.4	95.4	95.1	80.2	78.7	92.4	98.5		100	88.1	98.2
gz3L	95.4	95.4	95.1	80.2	78.7	92.4	98.5	100		88.1	98.2
gz21cl	89.6	89.6	89.3	79	76.8	89	89.3	88.1	88.1		89.6
adil.flesh	95.4	95.4	95.1	81.4	79.9	92.4	99.7	98.2	98.2	89.6	

Table 10

BLASTN 2.1.2 [Nov-13-2000]

Reference:
Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 984591695-10075-13605

Query=
(25 letters)

Database: nt
807,597 sequences; 2,863,827,885 total letters

If you have any problems or questions with the results of this search please refer to the BLAST FAQs

Taxonomy reports

Distribution of 500 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments

Sequences producing significant alignments:

	Score (bits)	E Value
gb|AF231651.1|AF231651 Strongylura notata clone HB-82 cytoc...	50	2e-05
gb|AF231650.1|AF231650 Strongylura notata clone HB-159 cyto...	50	2e-05
ref|NC_002672.1| Dinornis giganteus mitochondrion, complete...	50	2e-05
ref|NC_002673.1| Emeus crassus mitochondrion, complete genome	50	2e-05
gb|AF232015.1|AF232015 Nothrotheriops shastensis cytochrome...	50	2e-05
gb|AF232013.1|AF232013 Bradypus variegatus cytochrome b gen...	50	2e-05
gb|AY016015.1| Emeus crassus mitochondrion, complete genome	50	2e-05
gb|AY016013.1| Dinornis giganteus mitochondrion, complete g...	50	2e-05
gb|AY016014.1| Dromaius novaehollandiae mitochondrion, part...	50	2e-05
gb|AF230167.1|AF230167 Bonasa umbellus cytochrome b (CYTB) ...	50	2e-05
gb|AF074594.1|AF074594 Baeolophus bicolor cytochrome b gene...	50	2e-05
gb|AY005210.1| Poospiza melanoleuca isolate 3 cytochrome b ...	50	2e-05
gb|AY005209.1| Poospiza melanoleuca isolate 2 cytochrome b ...	50	2e-05
gb|AY005208.1| Poospiza melanoleuca isolate 1 cytochrome b ...	50	2e-05
gb|AY005205.1| Poospiza hispaniolensis cytochrome b (cytb) ...	50	2e-05
gb|AY005204.1| Poospiza garleppi cytochrome b (cytb) gene, ...	50	2e-05
gb|AY005203.1| Poospiza erythrophrys cytochrome b (cytb) ge...	50	2e-05
gb|AY005201.1| Poospiza boliviana cytochrome b (cytb) gene,...	50	2e-05
gb|AY005199.1| Poospiza alticola isolate 2 cytochrome b (cy...	50	2e-05
gb|AY005198.1| Poospiza alticola isolate 1 cytochrome b (cy...	50	2e-05
gb|AF155870.1|AF155870 Heterocephalus glaber cytochrome b (...	50	2e-05
gb|AF189123.1|AF189123 Glyptotermes eukalypti cytochrome b ...	50	2e-05
gb|AF102099.1|AF102099 Criniferoides leucogaster cytochrome...	50	2e-05
gb|AF102095.1|AF102095S1 Corythaixoides concolor cytochrome...	50	2e-05
gb|AF271065.1|AF271065 Mustela erminea specimen-voucher AF1...	50	2e-05
gb|AF243857.1|AF243857 Strongylura notata notata cytochrome...	50	2e-05
gb|AF243856.1|AF243856 Strongylura notata forsythia cytochr...	50	2e-05
ref|NC_001567.1| Bos taurus mitochondrion, complete genome	50	2e-05
gb|AF306872.1|AF306872 Brachyramphus marmoratus haplotype M...	50	2e-05
gb|AF306871.1|AF306871 Brachyramphus marmoratus haplotype M...	50	2e-05
gb|AF306870.1|AF306870 Brachyramphus brevirostris haplotype...	50	2e-05
gb|AF306869.1|AF306869 Brachyramphus brevirostris haplotype...	50	2e-05
gb|AF306868.1|AF306868 Brachyramphus brevirostris haplotype...	50	2e-05
gb|AF010406.1|AF010406 Ovis aries complete mitochondrial ge...	50	2e-05
gb|AF248662.1|AF248662 Gryllus campestris haplotype 2 cytoc...	50	2e-05
gb|AF248661.1|AF248661 Gryllus campestris haplotype 1 cytoc...	50	2e-05
gb|AF096462.1|AF096462 Rhipidura albicollis cytochrome b ge...	50	2e-05
gb|AF283644.1|AF283644 Elaphe obsoleta cytochrome b gene, c...	50	2e-05
gb|AF283643.1|AF283643 Elaphe obsoleta cytochrome b gene, c...	50	2e-05
gb|AF283642.1|AF283642 Elaphe obsoleta cytochrome b gene, c...	50	2e-05
gb|AF283641.1|AF283641 Elaphe obsoleta cytochrome b gene, c...	50	2e-05
gb|AF283640.1|AF283640 Elaphe obsoleta cytochrome b gene, c...	50	2e-05
gb|AF283639.1|AF283639 Elaphe obsoleta cytochrome b gene, c...	50	2e-05
gb|AF283637.1|AF283637 Elaphe obsoleta LSUMZ 45359 cytochro...	50	2e-05
gb|AF283636.1|AF283636 Elaphe obsoleta LSUMZ 44662 cytochro...	50	2e-05
gb|AF283635.1|AF283635 Elaphe obsoleta LSUMZ 40443 cytochro...	50	2e-05
gb|AF283634.1|AF283634 Elaphe obsoleta LSUMZ 44335 cytochro...	50	2e-05
gb|AF283633.1|AF283633 Elaphe obsoleta LSUMZ 42624 cytochro...	50	2e-05
gb|AF283632.1|AF283632 Elaphe obsoleta LSUMZ H1911 cytochro...	50	2e-05
gb|AF283631.1|AF283631 Elaphe obsoleta LSUMZ 41197 cytochro...	50	2e-05
gb|AF283630.1|AF283630 Elaphe obsoleta LSUMZ 41189 cytochro...	50	2e-05
gb|AF283629.1|AF283629 Elaphe obsoleta LSUMZ 41188 cytochro...	50	2e-05
gb|AF283628.1|AF283628 Elaphe obsoleta LSUMZ 41187 cytochro...	50	2e-05
gb|AF283627.1|AF283627 Elaphe obsoleta LSUMZ 41186 cytochro...	50	2e-05
gb|AF283626.1|AF283626 Elaphe obsoleta LSUMZ 40943 cytochro...	50	2e-05
gb|AF283625.1|AF283625 Elaphe obsoleta LSUMZ 37499 cytochro...	50	2e-05
gb|AF283624.1|AF283624 Elaphe obsoleta LSUMZ 44480 cytochro...	50	2e-05
gb|AF283623.1|AF283623 Elaphe obsoleta LSUMZ 44451 cytochro...	50	2e-05
gb|AF283622.1|AF283622 Elaphe obsoleta LSUMZ 40444 cytochro...	50	2e-05
gb|AF283621.1|AF283621 Elaphe obsoleta LSUMZ 39925 cytochro...	50	2e-05
gb|AF283620.1|AF283620 Elaphe obsoleta LSUMZ 39163 cytochro...	50	2e-05
gb|AF283619.1|AF283619 Elaphe obsoleta LSUMZ39162 cytochrom...	50	2e-05
gb|AF283618.1|AF283618 Elaphe obsoleta LSUMZ H15896 cytochr...	50	2e-05
gb|AF283617.1|AF283617 Elaphe obsoleta LSUMZ H15892 cytochr...	50	2e-05
gb|AF283616.1|AF283616 Elaphe obsoleta LSUMZ 15891 cytochro...	50	2e-05
gb|AF283615.1|AF283615 Elaphe obsoleta LSUMZ H15890 cytochr...	50	2e-05
gb|AF283614.1|AF283614 Elaphe obsoleta LSUMZ H15887 cytochr...	50	2e-05
gb|AF283613.1|AF283613 Elaphe obsoleta LSUMZ H15884 cytochr...	50	2e-05

Table 9. Animals selected for validation of minimum P'S score for efficient amplification of DNA templates in PCR

SL.	Name	P, S/AFF	P, S/AFR
1	Indian black buck (Antilope cervicapra)	97, 58	96, 54
2	Sheep (Ovis	87, 53	96, 54
3	Pig (*Sus scrofa*)	87, 52	87, 41
4	Fresh water dolphin (*Platanista gangetica*)	86, 49	82, 47

Sequences producing significant alignments:	Score (bits)	E Value
gb|AF231651.1|AF231651 Strongylura notata clone HB-82 cytoc...	50	2e-05
gb|AF231650.1|AF231650 Strongylura notata clone HB-159 cyto...	50	2e-05
ref|NC_002672.1| Dinornis giganteus mitochondrion, complete...	50	2e-05
ref|NC_002673.1| Emeus crassus mitochondrion, complete genome	50	2e-05
gb|AF232015.1|AF232015 Nothrotheriops shastensis cytochrome...	50	2e-05
gb|AF232013.1|AF232013 Bradypus variegatus cytochrome b gen...	50	2e-05
gb|AY016015.1| Emeus crassus mitochondrion, complete genome	50	2e-05
gb|AY016013.1| Dinornis giganteus mitochondrion, complete g...	50	2e-05
gb|AY016014.1| Dromaius novaehollandiae mitochondrion, part...	50	2e-05
gb|AF230167.1|AF230167 Bonasa umbellus cytochrome b (CYTB) ...	50	2e-05
gb|AF074594.1|AF074594 Baeolophus bicolor cytochrome b gene...	50	2e-05
gb|AY005210.1| Poospiza melanoleuca isolate 3 cytochrome b ...	50	2e-05
gb|AY005209.1| Poospiza melanoleuca isolate 2 cytochrome b ...	50	2e-05
gb|AY005208.1| Poospiza melanoleuca isolate 1 cytochrome b ...	50	2e-05
gb|AY005205.1| Poospiza hispaniolensis cytochrome b (cytb) ...	50	2e-05
gb|AY005204.1| Poospiza garleppi cytochrome b (cytb) gene, ...	50	2e-05
gb|AY005203.1| Poospiza erythrophrys cytochrome b (cytb) ge...	50	2e-05
gb|AY005201.1| Poospiza boliviana cytochrome b (cytb) gene,...	50	2e-05
gb|AY005199.1| Poospiza alticola isolate 2 cytochrome b (cy...	50	2e-05
gb|AY005198.1| Poospiza alticola isolate 1 cytochrome b (cy...	50	2e-05
gb|AF155870.1|AF155870 Heterocephalus glaber cytochrome b (...	50	2e-05
gb|AF189123.1|AF189123 Glyptotermes eukalypti cytochrome b ...	50	2e-05
gb|AF102099.1|AF102099 Criniferoides leucogaster cytochrome...	50	2e-05
gb|AF102095.1|AF102095S1 Corythaixoides concolor cytochrome...	50	2e-05
gb|AF271065.1|AF271065 Mustela erminea specimen-voucher AF1...	50	2e-05
gb|AF243857.1|AF243857 Strongylura notata notata cytochrome...	50	2e-05
gb|AF243856.1|AF243856 Strongylura notata forsythia cytochr...	50	2e-05
ref|NC_001567.1| Bos taurus mitochondrion, complete genome	50	2e-05
gb|AF306872.1|AF306872 Brachyramphus marmoratus haplotype M...	50	2e-05
gb|AF306871.1|AF306871 Brachyramphus marmoratus haplotype M...	50	2e-05
gb|AF306870.1|AF306870 Brachyramphus brevirostris haplotype...	50	2e-05
gb|AF306869.1|AF306869 Brachyramphus brevirostris haplotype...	50	2e-05
gb|AF306868.1|AF306868 Brachyramphus brevirostris haplotype...	50	2e-05
gb|AF010406.1|AF010406 Ovis aries complete mitochondrial ge...	50	2e-05
gb|AF248662.1|AF248662 Gryllus campestris haplotype 2 cytoc...	50	2e-05
gb|AF248661.1|AF248661 Gryllus campestris haplotype 1 cytoc...	50	2e-05
gb|AF096462.1|AF096462 Rhipidura albicollis cytochrome b ge...	50	2e-05
gb|AF283644.1|AF283644 Elaphe obsoleta cytochrome b gene, c...	50	2e-05
gb|AF283643.1|AF283643 Elaphe obsoleta cytochrome b gene, c...	50	2e-05
gb|AF283642.1|AF283642 Elaphe obsoleta cytochrome b gene, c...	50	2e-05
gb|AF283641.1|AF283641 Elaphe obsoleta cytochrome b gene, c...	50	2e-05
gb|AF283640.1|AF283640 Elaphe obsoleta cytochrome b gene, c...	50	2e-05
gb|AF283639.1|AF283639 Elaphe obsoleta cytochrome b gene, c...	50	2e-05
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gb|AF283633.1|AF283633 Elaphe obsoleta LSUMZ 42624 cytochro...	50	2e-05
gb|AF283632.1|AF283632 Elaphe obsoleta LSUMZ H1911 cytochro...	50	2e-05
gb|AF283631.1|AF283631 Elaphe obsoleta LSUMZ 41197 cytochro...	50	2e-05
gb|AF283630.1|AF283630 Elaphe obsoleta LSUMZ 41189 cytochro...	50	2e-05
gb|AF283629.1|AF283629 Elaphe obsoleta LSUMZ 41188 cytochro...	50	2e-05
gb|AF283628.1|AF283628 Elaphe obsoleta LSUMZ 41187 cytochro...	50	2e-05
gb|AF283627.1|AF283627 Elaphe obsoleta LSUMZ 41186 cytochro...	50	2e-05
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gb|AF283624.1|AF283624 Elaphe obsoleta LSUMZ 44480 cytochro...	50	2e-05
gb|AF283623.1|AF283623 Elaphe obsoleta LSUMZ 44451 cytochro...	50	2e-05
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gb|AF283620.1|AF283620 Elaphe obsoleta LSUMZ 39163 cytochro...	50	2e-05
gb|AF283619.1|AF283619 Elaphe obsoleta LSUMZ39162 cytochrom...	50	2e-05
gb|AF283618.1|AF283618 Elaphe obsoleta LSUMZ H15896 cytochr...	50	2e-05
gb|AF283617.1|AF283617 Elaphe obsoleta LSUMZ H15892 cytochr...	50	2e-05
gb|AF283616.1|AF283616 Elaphe obsoleta LSUMZ 15891 cytochro...	50	2e-05
gb|AF283615.1|AF283615 Elaphe obsoleta LSUMZ H15890 cytochr...	50	2e-05
gb|AF283614.1|AF283614 Elaphe obsoleta LSUMZ H15889 cytochr...	50	2e-05
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gb|AF283611.1|AF283611	Elaphe obsoleta LSUMZ H15031 cytochr...	50	2e-05
gb|AF283610.1|AF283610	Elaphe obsoleta LSUMZ H15030 cytochr...	50	2e-05
gb|AF283609.1|AF283609	Elaphe obsoleta CAS 169468 cytochrom...	50	2e-05
gb|AF283608.1|AF283608	Elaphe obsoleta LSUMZ H14782 cytochr...	50	2e-05
gb|AF283607.1|AF283607	Elaphe obsoleta LSUMZ H14781 cytochr...	50	2e-05
gb|AF283606.1|AF283606	Elaphe obsoleta LSUMZ H14724 cytochr...	50	2e-05
gb|AF283605.1|AF283605	Elaphe obsoleta cytochrome b gene, c...	50	2e-05
gb|AF283604.1|AF283604	Elaphe obsoleta cytochrome b gene, c...	50	2e-05
gb|AF283603.1|AF283603	Elaphe obsoleta cytochrome b gene, c...	50	2e-05
gb|AF283602.1|AF283602	Elaphe obsoleta LSUMZ H3388 cytochro...	50	2e-05
gb|AF283601.1|AF283601	Elaphe obsoleta LSUMZ H3385 cytochro...	50	2e-05
gb|AF283600.1|AF283600	Elaphe obsoleta LSUMZ H3384 cytochro...	50	2e-05
gb|AF283599.1|AF283599	Elaphe bairdi LSUMZ H3382 cytochrome...	50	2e-05
gb|AF283598.1|AF283598	Elaphe bairdi LSUMZ H3381 cytochrome...	50	2e-05
gb|AF283597.1|AF283597	Elaphe obsoleta LSUMZ H3379 cytochro...	50	2e-05
gb|AF283596.1|AF283596	Elaphe obsoleta LSUMZ 39816 cytochro...	50	2e-05
gb|AF283595.1|AF283595	Elaphe obsoleta LSUMZ H3376 cytochro...	50	2e-05
gb|AF283594.1|AF283594	Elaphe obsoleta LSUMZ H3345 cytochro...	50	2e-05
gb|AF283593.1|AF283593	Elaphe obsoleta LSUMZ H3309 cytochro...	50	2e-05
gb|AF283592.1|AF283592	Elaphe obsoleta LSUMZ H3306 cytochro...	50	2e-05
gb|AF283591.1|AF283591	Elaphe obsoleta LSUMZ H3276 cytochro...	50	2e-05
gb|AF283590.1|AF283590	Elaphe obsoleta LSUMZ H3246 cytochro...	50	2e-05
gb|AF283589.1|AF283589	Elaphe obsoleta LSUMZ H3212 cytochro...	50	2e-05
gb|AF283588.1|AF283588	Elaphe obsoleta LSUMZ H3209 cytochro...	50	2e-05
gb|AF283587.1|AF283587	Elaphe obsoleta LSUMZ H3206 cytochro...	50	2e-05
gb|AF283586.1|AF283586	Elaphe obsoleta LSUMZ H3191 cytochro...	50	2e-05
gb|AF283585.1|AF283585	Elaphe obsoleta LSUMZ H3190 cytochro...	50	2e-05
gb|AF283584.1|AF283584	Elaphe obsoleta LSUMZ H3189 cytochro...	50	2e-05
gb|AF283583.1|AF283583	Elaphe obsoleta LSUMZ H3188 cytochro...	50	2e-05
gb|AF283582.1|AF283582	Elaphe obsoleta LSUMZ H3186 cytochro...	50	2e-05
gb|AF283581.1|AF283581	Elaphe obsoleta LSUMZ H3169 cytochro...	50	2e-05
gb|AF283580.1|AF283580	Elaphe obsoleta CAS 203083 cytochrom...	50	2e-05
gb|AF283579.1|AF283579	Elaphe obsoleta CAS 203079 cytochrom...	50	2e-05
gb|AF283578.1|AF283578	Elaphe obsoleta LSUMZ H2286 cytochro...	50	2e-05
gb|AF283577.1|AF283577	Elaphe obsoleta CAS 208631 cytochrom...	50	2e-05
gb|AF283576.1|AF283576	Elaphe obsoleta LSUMZ H2229 cytochro...	50	2e-05
gb|AF187030.1|AF187030	Rhinophylla pumilio isolate TK46001 ...	50	2e-05
gb|AF310052.1|AF310052	Poospiza hispaneolensis cytochrome b...	50	2e-05
gb|AF310046.1|AF310046	Volatinia jacarina cytochrome b gene...	50	2e-05
gb|AF171919.1|AF171919	Deinagkistrodon acutus cytochrome b ...	50	2e-05
gb|AF171897.1|AF171897	Trimeresurus mucrosquamatus cytb gen...	50	2e-05
gb|AF290174.1|AF290174	Agelaius cyanopus cytochrome b (cytb...	50	2e-05
gb|AF290173.1|AF290173	Agelaius phoeniceus cytochrome b (cy...	50	2e-05
gb|AF290171.1|AF290171	Quiscalus major cytochrome b (cytb) ...	50	2e-05
gb|AF290170.1|AF290170	Amblycercus holosericeus cytochrome ...	50	2e-05
gb|AF290150.1|AF290150	Volatinia jacarina cytochrome b (cyt...	50	2e-05
gb|AF176252.1|AF176252	Reithrodontomys zacatecae cytochrome...	50	2e-05
gb|AF176251.1|AF176251	Reithrodontomys zacatecae cytochrome...	50	2e-05
gb|AF163907.1|AF163907	Microtus xanthognathus cytochrome b ...	50	2e-05
gb|AF163904.1|AF163904	Microtus pinetorum cytochrome b gene...	50	2e-05
gb|AF163901.1|AF163901	Microtus ochrogaster cytochrome b ge...	50	2e-05
gb|AF163899.1|AF163899	Microtus miurus cytochrome b gene, c...	50	2e-05
gb|AF163891.1|AF163891	Microtus californicus cytochrome B (...	50	2e-05
gb|AF163890.1|AF163890	Microtus abbreviatus cytochrome B (c...	50	2e-05
gb|AF288524.1|AF288524	Dipsochelys dussumieri isolate Germa...	50	2e-05
gb|AF288523.1|AF288523	Dipsochelys dussumieri isolate white...	50	2e-05
gb|AF288522.1|AF288522	Dipsochelys dussumieri isolate Aldy ...	50	2e-05
gb|AF123530.1|AF123530	Psilopogon pyrolophus cytochrome b (...	50	2e-05
gb|AF123512.1|AF123512	Eubucco bourcierii tucinkae cytochro...	50	2e-05
gb|AF206548.1|AF206548	Adolfus vaueraselli cytochrome b gen...	50	2e-05
gb|AF197867.1|AF197867	Cymnorhina tibicen cytochrome b gene...	50	2e-05
gb|U63197.2|SEU63197	Sitta europaea cytochrome b gene, part...	50	2e-05
ref|NC_001945.1|	Dinodon semicarinatus mitochondrion, compl...	50	2e-05
ref|NC_001821.1|	Dasypus novemcinctus mitochondrion, comple...	50	2e-05
gb|AF141217.1|AF141217	Dasymys incomtus country Tanzania cy...	50	2e-05
gb|AF201615.1|AF201615	Pantodon buchholzi cytochrome b gene...	50	2e-05
gb|AF077920.1|AF077920	Bombus nevadensis cytochrome b gene....	50	2e-05
gb|AF190612.1|AF190612	Oreamnos americanus cytochrome b (cy...	50	2e-05
gb|J01394.1|BOVMT	Bos taurus mitochondrion, complete genome	50	2e-05
gb|AF191810.1|AF191810	Cochlearius cochlearius cytochrome b...	50	2e-05

gb|U89181.1|CAU89181	Chlorostilbon aureoventris cytochrome ...	50	2e-05
gb|U89171.1|AFU89171	Asio flammeus cytochrome b (cytb) gene...	50	2e-05
gb|AF217833.1|AF217833	Homoroselaps lacteus cytochrome b ge...	50	2e-05
gb|AF217822.1|AF217822	Hydrophis semperi cytochrome b gene,...	50	2e-05
gb|AF217813.1|AF217813	Acanthophis antarcticus cytochrome b...	50	2e-05
gb|AF220408.1|AF220408	Calliophis kelloggi cytochrome b (cy...	50	2e-05
gb|AF126430.1|AF126430	Ellobius fuscocapillus cytochrome b ...	50	2e-05
gb|AF090337.1|AF090337	Aythya americana mitochondrion, comp...	50	2e-05
gb|AF059111.1|AF059111	Sarkidiornis melanotos cytochrome b ...	50	2e-05
gb|AF059053.1|AF059053	Aix sponsa cytochrome b gene, partia...	50	2e-05
gb|AF099308.1|AF099308	Icterus wagleri wagleri cytochrome b...	50	2e-05
gb|AF099295.1|AF099295	Icterus gularis yucatanensis cytochr...	50	2e-05
gb|AF099294.1|AF099294	Icterus gularis tamaulipensis cytoch...	50	2e-05
gb|AF099293.1|AF099293	Icterus gularis gularis cytochrome b...	50	2e-05
gb|AF160610.1|AF160610	Cricetomys emini Cemi636 cytochrome ...	50	2e-05
gb|AF036280.1|AF036280	Tragelaphus strepsiceros cytochrome ...	50	2e-05
gb|AF036277.1|AF036277	Tragelaphus scriptus cytochrome b (c...	50	2e-05
gb|AF036274.1|	Tetracerus quadricornis cytochrome b (cytb) ...	50	2e-05
gb|AF194218.1|AF194218	Phrynosoma platyrhinos cytochrome b ...	50	2e-05
gb|AF194216.1|AF194216	Urosaurus ornatus cytochrome b gene,...	50	2e-05
ref|NC_002009.1|	Artibeus jamaicensis mitochondrion, comple...	50	2e-05
ref|NC_001941.1|	Ovis aries mitochondrion, complete genome	50	2e-05
ref|NC_000877.1|	Aythya americana mitochondrion, complete g...	50	2e-05
ref|NC_000846.1|	Rhea americana mitochondrion, complete genome	50	2e-05
gb|U27551.1|GCU27551	Grus canadensis tabida cytochrome b (c...	50	2e-05
gb|AF089058.1|AF089058	Quiscalus quiscula cytochrome b (cyt...	50	2e-05
gb|AF089055.1|AF089055	Quiscalus major cytochrome b (cytb) ...	50	2e-05
gb|AF089054.1|AF089054	Quiscalus lugubris cytochrome b (cyt...	50	2e-05
gb|AF089046.1|AF089046	Oreopsar bolivianus cytochrome b (cy...	50	2e-05
gb|AF089042.1|AF089042	Molothrus badius cytochrome b (cytb)...	50	2e-05
gb|AF089039.1|AF089039	Macroagelaius imthurni cytochrome b ...	50	2e-05
gb|AF089037.1|AF089037	Lampropsar tanagrinus cytochrome b (...	50	2e-05
gb|AF089026.1|AF089026	Gymnomystax mexicanus cytochrome b (...	50	2e-05
gb|AF089025.1|AF089025	Gnorimopsar chopi cytochrome b (cytb...	50	2e-05
gb|AF089024.1|AF089024	Euphagus cyanocephalus cytochrome b ...	50	2e-05
gb|AF089023.1|AF089023	Euphagus carolinus cytochrome b (cyt...	50	2e-05
gb|AF089021.1|AF089021	Dives warszewiczi cytochrome b (cyt...	50	2e-05
gb|AF089020.1|AF089020	Curaeus curaeus cytochrome b (cytb) ...	50	2e-05
gb|AF089016.1|AF089016	Amblycercus holosericeus cytochrome ...	50	2e-05
gb|AF089013.1|AF089013	Agelaius xanthophthalmus cytochrome ...	50	2e-05
gb|AF089012.1|AF089012	Agelaius xanthomus cytochrome b (cyt...	50	2e-05
gb|AF089008.1|AF089008	Agelaius phoeniceus sub-species phoe...	50	2e-05
gb|AF089006.1|AF089006	Agelaius humeralis cytochrome b (cyt...	50	2e-05
gb|AF089005.1|AF089005	Agelaius cyanopus cytochrome b (cytb...	50	2e-05
gb|AF108696.1|AF108696	Scolomys juruaense cytochrome B (cyt...	50	2e-05
gb|AF108685.1|AF108685	Wiedomys pyrrhorhinos cytochrome B (...	50	2e-05
gb|AF108677.1|AF108677	Thomasomys oreas cytochrome B (cytB)...	50	2e-05
gb|AF145531.1|AF145531	Melanoplus foedus cytochrome b gene,...	50	2e-05
gb|AF145511.1|AF145511	Melanoplus angustipennis cytochrome ...	50	2e-05
gb|U89627.1|BMU89627	Bolitoglossa marmorea cytochrome b (cy...	50	2e-05
gb|U89623.1|BPU89623	Batrachoseps pacificus cytochrome b (c...	50	2e-05
gb|AF181470.1|AF181470	Okapia johnstoni cytochrome b gene, ...	50	2e-05
gb|AF084075.1|AF084075	Lagenorhynchus acutus cytochrome b g...	50	2e-05
gb|U90303.1|OMU90303	Ovibos moschatus cytochrome b (cytb) g...	50	2e-05
gb|U90302.1|OMU90302	Ovibos moschatus cytochrome b (cytb) g...	50	2e-05
gb|U90301.1|OMU90301	Ovibos moschatus cytochrome b (cytb) g...	50	2e-05
gb|U90300.1|OMU90300	Ovibos moschatus cytochrome b (cytb) g...	50	2e-05
gb|AF038883.1|AF038883	Deinagkistrodon acutus cytochrome b ...	50	2e-05
gb|AF039268.1|AF039268	Agkistrodon contortrix cytochrome b ...	50	2e-05
gb|AF039267.1|AF039267	Boa constrictor cytochrome b (cytb) ...	50	2e-05
gb|S49215.1|S49215	apocytochrome b [sheep, domestic, Merino...	50	2e-05
gb|AF158698.1|AF158698	Geomys pinetis cytochrome b gene, co...	50	2e-05
gb|AF158692.1|AF158692	Geomys bursarius jugoasicularis cyto...	50	2e-05
gb|AF068193.1|AF068193	Ithaginis cruentus cytochrome b (cyt...	50	2e-05
gb|AF091629.1|AF091629	Antilocapra americana cytochrome b (...	50	2e-05
gb|AF022063.1|	Tragelaphus strepsiceros cytochrome b (cytb) ...	50	2e-05
gb|AF022062.1|	Tragelaphus derbianus cytochrome b (cytb) ge...	50	2e-05
gb|AF022060.1|	Hippotragus equinus cytochrome b (cytb) gene...	50	2e-05
gb|AF022057.1|	Tragelaphus oryx cytochrome b (cytb) gene, m...	50	2e-05
gb|AF111500.1|AF111500	Lagenorhynchus acutus isolate LAC94...	50	2e-05
gb|AF111499.1|AF111499	Lagenorhynchus acutus isolate LAC93...	50	2e-05

gb|U69645.1|LBU69645	Loxocemus bicolor cytochrome b (cytb) ...	50	2e-05
gb|U69810.1|EMU69810	Eunectes notaeus cytochrome b (cytb) g...	50	2e-05
gb|U69808.1|EMU69808	Eunectes murinus cytochrome b (cytb) g...	50	2e-05
gb|U69799.1|ESU69799	Epicrates striatus fosteri cytochrome ...	50	2e-05
gb|U69796.1|ESU69796	Epicrates striatus strigilatus cytochr...	50	2e-05
gb|U69795.1|ESU69795	Epicrates striatus strigilatus cytochr...	50	2e-05
gb|U69794.1|ESU69794	Epicrates striatus monensis cytochrom...	50	2e-05
gb|U69793.1|ESU69793	Epicrates striatus monensis cytochrom...	50	2e-05
gb|U69792.1|EMU69792	Epicrates monensis cytochrome b (cytb)...	50	2e-05
gb|U69790.1|EMU69790	Epicrates monensis cytochrome b (cytb)...	50	2e-05
gb|U69786.1|EFU69786	Epicrates fordi cytochrome b (cytb) ge...	50	2e-05
gb|U69784.1|EFU69784	Epicrates fordi cytochrome b (cytb) ge...	50	2e-05
gb|U69779.1|ECU69779	Epicrates cenchria cytochrome b (cytb)...	50	2e-05
gb|U69777.1|ECU69777	Epicrates cenchria cytochrome b (cytb)...	50	2e-05
gb|U69776.1|EAU69776	Epicrates angulifer cytochrome b (cytb...	50	2e-05
gb|U69774.1|EAU69774	Epicrates angulifer cytochrome b (cytb...	50	2e-05
gb|U69772.1|CEU69772	Corallus enydris cytochrome b (cytb) g...	50	2e-05
gb|U69771.1|CEU69771	Corallus enydris cytochrome b (cytb) g...	50	2e-05
gb|U69770.1|CEU69770	Corallus enydris cytochrome b (cytb) g...	50	2e-05
gb|U69769.1|CEU69769	Corallus enydris cytochrome b (cytb) g...	50	2e-05
gb|U69752.1|CAU69752	Candoia aspera cytochrome b (cytb) gen...	50	2e-05
gb|U69746.1|BCU69746	Boa constrictor cytochrome b (cytb) ge...	50	2e-05
gb|U69740.1|BCU69740	Boa constrictor cytochrome b (cytb) ge...	50	2e-05
gb|AF139057.1|AF139057	Isoodon macrourus cytochrome b gene,...	50	2e-05
gb|AF090339.1|AF090339	Rhea americana mitochondrion, comple...	50	2e-05
gb|AF006275.1|AF006275	Chemidophorus tigris strain Isla Ang...	50	2e-05
gb|AF006267.1|AF006267	Chemidophorus tigris strain Isla Smi...	50	2e-05
gb|AF034969.1|AF034969	Connochaetes taurinus cytochrome b g...	50	2e-05
gb|AF028822.1|AF028822	Alcelaphus buselaphus cytochrome b g...	50	2e-05
gb|AF028821.1|AF028821	Damaliscus lunatus cytochrome b gene...	50	2e-05
gb|AF061340.1|AF061340	Artibeus jamaicensis mitochondrial D...	50	2e-05
gb|AF076093.1|AF076093	Thalassarche impavida cytochrome b (...	50	2e-05
gb|AF076091.1|AF076091	Thalassarche carteri cytochrome b (c...	50	2e-05
gb|AF076072.1|AF076072	Pelagodroma marina cytochrome b (cyt...	50	2e-05
gb|AF076063.1|AF076063	Oceanodroma furcata cytochrome b (cy...	50	2e-05
gb|AF076059.1|AF076059	Hydrobates pelagicus cytochrome b (c...	50	2e-05
gb|AF076056.1|AF076056	Garrodia nereis cytochrome b (cytb) ...	50	2e-05
gb|AF076053.1|AF076053	Fregetta tropica cytochrome b (cytb)...	50	2e-05
gb|AF076050.1|AF076050	Diomedea gibsoni cytochrome b (cytb)...	50	2e-05
gb|AF076049.1|AF076049	Diomedea epomophora cytochrome b (cy...	50	2e-05
gb|AF076048.1|AF076048	Diomedea chionoptera cytochrome b (c...	50	2e-05
gb|AF076047.1|AF076047	Diomedea antipodensis cytochrome b (...	50	2e-05
gb|U83314.1|MSU83314	Micrastur semitorquatus cytochrome b (...	50	2e-05
gb|U83318.1|MEU83318	Microhierax erythrogenys cytochrome b ...	50	2e-05
gb|U37303.1|SAU37303	Synthliboramphus antiquus cytochrome b...	50	2e-05
gb|U37302.1|PAU37302	Ptychoramphus aleuticus cytochrome b g...	50	2e-05
gb|U37296.1|CPU37296	Cyclorrhynchus psittacula cytochrome b...	50	2e-05
gb|U37289.1|BBU37289	Brachyramphus brevirostris cytochrome ...	50	2e-05
gb|U37286.1|APU37286	Aethia pygmaea cytochrome b gene, mito...	50	2e-05
gb|U37104.1|APU37104	Aethia pusilla cytochrome b gene, mito...	50	2e-05
gb|U37087.1|ACU37087	Aethia cristatella cytochrome b gene, ...	50	2e-05
gb|U87525.1|HGU87525	Heterocephalus glaber cytochrome-b gen...	50	2e-05
gb|U87524.1|HGU87524	Heterocephalus glaber cytochrome-b gen...	50	2e-05
gb|U87523.1|HGU87523	Heterocephalus glaber cytochrome-b gen...	50	2e-05
gb|U87522.1|HGU87522	Heterocephalus glaber cytochrome-b gen...	50	2e-05
gb|U17864.1|STU17864	Saiga tatarica cytochrome b gene, mito...	50	2e-05
gb|U17863.1|OAU17863	Oreamnos americanus cytochrome b gene....	50	2e-05
gb|U17862.1|OMU17862	Ovibos moschatus moschatus cytochrome ...	50	2e-05
gb|U17860.1|ODU17860	Ovis dalli cytochrome b gene, mitochon...	50	2e-05
gb|U17859.1|OCU17859	Ovis canadensis cytochrome b gene, mit...	50	2e-05
gb|U65274.1|TBU65274	Thomomys bottae cytochrome b (cytb) ge...	50	2e-05
gb|U65267.1|TBU65267	Thomomys bottae cytochrome b (cytb) ge...	50	2e-05
gb|U65260.1|TBU65260	Thomomys bottae cytochrome b (cytb) ge...	50	2e-05
gb|U65101.1|PAU65101	Perognathus amplus cytochrome b (cytb)...	50	2e-05
gb|AF034739.1|AF034739	Capra aegagrus cytochrome b (cytb) g...	50	2e-05
gb|AF034738.1|	Capra caucasica cytochrome b (cytb) gene, mi...	50	2e-05
gb|AF034737.1|	Capra cylindricornis cytochrome b (cytb) gen...	50	2e-05
gb|AF034736.1|AF034736	Capra falconeri cytochrome b (cytb) ...	50	2e-05
gb|AF034735.1|	Capra ibex cytochrome b (cytb) gene, mitocho...	50	2e-05
gb|AF034730.1|AF034730	Ovis aries cytochrome b (cytb) gene,...	50	2e-05
gb|AF034729.1|AF034729	Ovis vignei cytochrome b (cytb) gene	50	2e-05

gb|AF034724.1|	Ovis dalli dalli cytochrome b (cytb) gene, m...	50	2e-05
gb|AF034727.1|	Ovis ammon darwini cytochrome b (cytb) gene....	50	2e-05
gb|AF034724.1|AF034724	Pantholops hodgsoni cytochrome b (cy...	50	2e-05
gb|AF057132.1|AF057132	Taxidea taxus cytochrome b (cytb) ge...	50	2e-05
gb|U94805.1|TMU94805	Trogon melanurus cytochrome b gene, mi...	50	2e-05
gb|U94804.1|TCU94804	Trogon comptus cytochrome b gene, mito...	50	2e-05
gb|U94803.1|TVU94803	Trogon viridis cytochrome b gene, mito...	50	2e-05
gb|AF006251.1|AF006251	Sericossypha albocristata cytochrome...	50	2e-05
gb|AF006249.1|AF006249	Pyrrhocoma ruficeps cytochrome b (cy...	50	2e-05
gb|AF006238.1|AF006238	Lamprospiza melanoleuca cytochrome b...	50	2e-05
gb|AF006234.1|AF006234	Hemispingus atropileus cytochrome b ...	50	2e-05
gb|AF006226.1|AF006226	Cypsnagra hirundinacea cytochrome b ...	50	2e-05
gb|AF006215.1|AF006215	Chlorophanes spita cytochrome b (cyt...	50	2e-05
gb|AF006214.1|AF006214	Chlorochrysa calliparaea cytochrome ...	50	2e-05
gb|AF006213.1|AF006213	Calochaetes coccineus cytochrome b (...	50	2e-05
gb|AF006212.1|AF006212	Buthraupis montana cytochrome b (cyt...	50	2e-05
emb|AJ293419.1|RRU293419	Rupicapra rupicapra rupicapra mito...	50	2e-05
emb|AJ293416.1|RPY293416	Rupicapra pyrenaica pyrenaica mito...	50	2e-05
emb|AJ293415.1|RPY293415	Rupicapra pyrenaica parva mitochon...	50	2e-05
emb|AJ293414.1|RPY293414	Rupicapra pyrenaica ornata mitocho...	50	2e-05
emb|AJ293412.1|RRU293412	Rupicapra rupicapra rupicapra mito...	50	2e-05
emb|AJ293418.1|CFA293418	Capra falconeri mitochondrial part...	50	2e-05
gb|U07578.1|DCU07578	Dasycercus cristicauda mitochondrion c...	50	2e-05
emb|AJ004180.1|HPAJ4180	Hydrobates pelagicus mitochondrial ...	50	2e-05
emb|Y15695.1|SMY15695	Schilbe mystus mitochondrial cytb gen...	50	2e-05
emb|Y15697.1|EDY15697	Eutropius depressirostris mitochondri...	50	2e-05
emb|Y15696.1|EDY15696	Eutropius depressirostris mitochondri...	50	2e-05
gb|AF015035.1|AF015035	Steatocranus casuarinus 20 cytochrom...	50	2e-05
gb|AF015761.1|AF015761	Palmeria dolei cytochrome b (Cytb) g...	50	2e-05
gb|AF015758.1|AF015758	Oreomystis mana cytochrome b (Cytb) ...	50	2e-05
gb|AF015756.1|AF015756	Vestiaria coccinea cytochrome b (Cyt...	50	2e-05
gb|AF015754.1|AF015754	Himatione sanguinea cytochrome b (Cy...	50	2e-05
gb|U76052.1|DNU76052	Dromaius novaehollandiae cytochrome b ...	50	2e-05
emb|AJ236834.1|CGL236834	Clethrionomys glareolus mitochondr...	50	2e-05
gb|U83158.1|POU83158	Pelecanus onocrotalus cytochrome B gen...	50	2e-05
gb|U83157.1|POU83157	Pelecanus onocrotalus cytochrome B gen...	50	2e-05
gb|U83156.1|AAU83156	Anhinga anhinga cytochrome B gene, mit...	50	2e-05
gb|U83155.1|AAU83155	Anhinga anhinga cytochrome B gene, mit...	50	2e-05
gb|U83154.1|AAU83154	Anhinga anhinga cytochrome B gene, mit...	50	2e-05
gb|U81356.1|CLU81356	Chelodina longicollis cytochrome b gen...	50	2e-05
emb|AJ277676.1|ESC277676	Elaphe scalaris mitochondrial part...	50	2e-05
emb|AJ277675.1|ESC277675	Elaphe scalaris mitochondrial part...	50	2e-05
emb|AJ277672.1|ELO277672	Elaphe longissima mitochondrial pa...	50	2e-05
emb|AJ277671.1|ELO277671	Elaphe longissima mitochondrial pa...	50	2e-05
emb|Y11832.1|MTDNCOMGN	Dasypus novemcinctus complete mitoch...	50	2e-05
emb|AJ388467.1|NBA388467	Nemacheilus barbatulus mitchondria...	50	2e-05
emb|AJ388468.1|IME388468	Ictalurus melas mitchondrial cyt b...	50	2e-05
emb|AJ388459.1|LDE388459	Leucaspius delineatus mitchondrial...	50	2e-05
gb|U46167.1|SCU46167	Sciurus carolinensis cytochrome b gene...	50	2e-05
emb|AJ245673.1|SIN245673	Schilbe intermedius partial mitoch...	50	2e-05
emb|AJ245638.1|SIN245638	Schilbe intermedius partial mitoch...	50	2e-05
emb|AJ245678.1|EDE245678	Eutropius depressirostris partial ...	50	2e-05
emb|AJ245677.1|EDE245677	Eutropius depressirostris partial ...	50	2e-05
emb|AJ245676.1|EDE245676	Eutropius depressirostris partial ...	50	2e-05
emb|AJ245675.1|EDE245675	Eutropius depressirostris partial ...	50	2e-05
emb|AJ245674.1|EDE245674	Eutropius depressirostris partial ...	50	2e-05
emb|Y16886.3|MTRACOMPL	Rhea americana complete mitochondria....	50	2e-05
gb|U60768.1|PCU60768	Parus cinctus cytochrome b gene, mitoc...	50	2e-05
gb|U48955.1|TMU48955	Thalassarche melanophris melanophris c...	50	2e-05
gb|U48954.1|TCU48954	Thalassarche chrysostoma cytochrome b ...	50	2e-05
gb|U48944.1|TCU48944	Thalassarche chlororhynchos chlororhyn...	50	2e-05
gb|U48943.1|PPU48943	Phoebetria palpebrata cytochrome b (cy...	50	2e-05
gb|U48942.1|PFU48942	Phoebetria fusca cytochrome b (cytb) g...	50	2e-05
gb|U48941.1|MGU48941	Macronectes giganteus cytochrome b (cy...	50	2e-05
gb|U48947.1|DEU48947	Diomedea exulans dabbenena cytochrome ...	50	2e-05
gb|U48946.1|DEU48946	Diomedea epomophora sanfordi cytochrom...	50	2e-05
gb|U48948.1|DAU48948	Diomedea amsterdamensis cytochrome b (...	50	2e-05
gb|U15725.1|PRU15725	Piranga rubra cytochrome b gene, mitoc...	50	2e-05
gb|U66508.1|APU66508	Artibeus planirostris cytochrome b (cy...	50	2e-05
gb|U66507.1|AOU66507	Artibeus obscurus cytochrome b (cytb) ...	50	2e-05
gb|U66506.1|AOU66506	Artibeus obscurus cytochrome b (cytb) ...	50	2e-05

gb|U66505.1|ALU66505	Artibeus lituratus cytochrome b (cytb)...	50	2e-05
gb|U66504.1|AJU66504	Artibeus jamaicensis cytochrome b (cyt...	50	2e-05
gb|U66503.1|AJU66503	Artibeus jamaicensis cytochrome b (cyt...	50	2e-05
gb|U66502.1|AIU66502	Artibeus intermedius cytochrome b (cyt...	50	2e-05
gb|U66501.1|AIU66501	Artibeus inopinatus cytochrome b (cytb...	50	2e-05
gb|U66500.1|AHU66500	Artibeus hirsutus cytochrome b (cytb) ...	50	2e-05
gb|U66499.1|AFU66499	Artibeus fraterculus cytochrome b (cyt...	50	2e-05
gb|U66498.1|AFU66498	Artibeus fimbriatus cytochrome b (cytb...	50	2e-05
gb|U63061.1|BBU63061	Brachyramphus brevirostris cytochrome ...	50	2e-05
gb|U63060.1|BBU63060	Brachyramphus brevirostris cytochrome ...	50	2e-05
gb|U63059.1|BBU63059	Brachyramphus brevirostris cytochrome ...	50	2e-05
gb|U63058.1|BBU63058	Brachyramphus brevirostris cytochrome ...	50	2e-05
gb|U58386.1|SJU58386	Scolomys juruaense cytochrome b (cyt-b...	50	2e-05
gb|L11905.1|CGYMTCYTBD	Cratogeomys gymnurus mitochondrial c...	50	2e-05
gb|U34672.1|MNU34672	Metachirus nudicaudatus cytochrome b l...	50	2e-05
gb|U34671.1|MNU34671	Metachirus nudicaudatus cytochrome b l...	50	2e-05
emb|Y14951.1|MTY14951	Capreolus capreolus mitochondrial cyt...	50	2e-05
emb|Y14371.1|MTCCCYTB	Capreolus capreolus mitochondrial cyt...	50	2e-05
gb|L11909.1|CGYMTCYTBH	Cratogeomys tylorhinus mitochondrial...	50	2e-05
gb|L11901.1|PPGMTCYTBB	Geomys bursarius juggosicularis mito...	50	2e-05
gb|L11904.1|CGYMTCYTBC	Cratogeomys goldmani goldmani mitoch...	50	2e-05
emb|X94928.1|SPCYTB	S.putorius mitochondrial DNA for cytoch...	50	2e-05
gb|U46770.1|ARU46770	Anthus richardi cytochrome b gene, mit...	50	2e-05
gb|U46769.1|ABU46769	Anthus berthelotii cytochrome b gene, ...	50	2e-05
gb|U46183.1|SSU46183	Sciurus stramineus cytochrome b gene, ...	50	2e-05
emb|Y10728.1|PSMY10728	P.schwarzi mitochondrial cytb gene, ...	50	2e-05
emb|X95768.1|NLMCB	N.leucopterus mitochondrial cytochrome b...	50	2e-05
emb|X95767.1|NGRIMCB	N.griseus mitochondrial cytochrome b gene	50	2e-05
emb|X86763.1|MTVGCYT26	V.gryphus mitochondrial cytb gene	50	2e-05
emb|X86754.1|MTLCCYT17	L.crumeniferus mitochondrial cytb gene	50	2e-05
emb|X86743.1|MTCACYT6	C.aura mitochondrial cytb gene	50	2e-05
dbj|AB035242.1|AB035242	Pantodon buchholzi mitochondrial cy...	50	2e-05
emb|X60946.1|MITDCB33	T. dorbignyi mitochondrial gene for c...	50	2e-05
emb|AJ000029.1|MIRTCYB29	Rangifer tarandus mitochondrial cy...	50	2e-05
emb|X82302.1|MIPFCYTBG	P.fasciata mitochondrial cytochrome ...	50	2e-05
emb|X56291.1|MIOHCYTB	O.hemionus mitochondrion cytb gene fo...	50	2e-05
emb|X56284.1|MIOACYTB	O.aries mitochondrion cytb gene for c...	50	2e-05
emb|AJ000022.1|MIMSCYB22	Dama dama mitochondrial cytb gene	50	2e-05
emb|X72005.1|MILWCYTB	L.weddelli mitochondrial gene for cyt...	50	2e-05
emb|Y08814.1|MIHLCYTBG	H.liberiensis mitochondrial cytochro...	50	2e-05
emb|X60942.1|MIGTCB33	Gymnorhina tibicen mitochondrial gene...	50	2e-05
emb|X56290.1|MIDDCYTB	D.dama mitochondrion cytb gene for cy...	50	2e-05
emb|AJ000021.1|MICECYB21	Cervus elaphus mitochondrial cytb ...	50	2e-05
emb|AJ000024.1|MICCCYB24	Capreolus capreolus mitochondrial ...	50	2e-05
emb|V00654.1|MIBTXX	Bos taurus complete mitochondrial genome	50	2e-05
emb|X56286.1|MIAACYTBA	A.americana mitochondrion cytb gene ...	50	2e-05
gb|L19718.1|AJUMTCYTB	Artibeus lituratus mitochondrial cyto...	50	2e-05
gb|U27543.1|BRU27543	Balearica regulorum cytochrome b (cytb...	50	2e-05
dbj|AB030025.1|AB030025	Sciurus stramineus mitochondrial cy...	50	2e-05
gb|U18258.1|SCU18258	Spharagemon campestris cytochrome b ge...	50	2e-05
gb|U18257.1|SCU18257	Spharagemon collare cytochrome b gene,...	50	2e-05
gb|U18253.1|TPU18253	Trimerotropis pistrinaria cytochrome b...	50	2e-05
gb|U18250.1|CPU18250	Camnula pellucida cytochrome b gene, m...	50	2e-05
gb|U17904.1|CCU17904	Circotettix carlinianus mitochondrion ...	50	2e-05
dbj|D84202.1|GOTMTCB8	Capra falconeri mitochondrial DNA for...	50	2e-05
dbj|D82889.1|D82889	Bos javanicus mitochondrial DNA for cyt...	50	2e-05
dbj|D32195.1|CCRMTCB25	Capricornis sumatrensis mitochodrial...	50	2e-05
dbj|D32191.1|CCRMTCB21	Capricornis crispus mitochondrial ge...	50	2e-05
dbj|AB021098.1|AB021098	Cervus elaphus kansuensis mitochond...	50	2e-05
dbj|AB021097.1|AB021097	Cervus elaphus xanthopygus mitochon...	50	2e-05
dbj|AB021095.1|AB021095	Cervus nippon yesoensis mitochondri...	50	2e-05
dbj|AB021094.1|AB021094	Cervus nippon centralis mitochondri...	50	2e-05
dbj|AB021092.1|AB021092	Cervus nippon mageshimae mitochondr...	50	2e-05
dbj|AB021091.1|AB021091	Cervus nippon keramae mitochondrial...	50	2e-05
dbj|AB001612.1|AB001612	Cervus elaphus mitochondrial DNA fo...	50	2e-05
dbj|D84205.1|SHPMTCB8	Sheep mitochondrial DNA for cytochrom...	50	2e-05
dbj|D84203.1|SHPMTCBC	Ovis musimon mitochondrial DNA for cy...	50	2e-05
dbj|D14616.1|BOVMTCB8	Bos javanicus mitochondrial gene for ...	50	2e-05
dbj|D14615.1|BOVMTCBA	Bovine mitochondrial gene for cytochr...	50	2e-05
dbj|D32198.1|ORMMTCB28	Oreamnos americanus mitochondrial ge...	50	2e-05
dbj|D32196.1|NAOMTCB26	Nemorhaedus goral mitochondrial gene...	50	2e-05

dbj|D32192.1|CEUMTCB22	Cervus nippon mitochondrial gene for...	50	2e-05
dbj|AB021095.1|AB021095	Cervus elaphus scoticus mitochondri...	50	2e-05
dbj|AB021096.1|AB021096	Cervus elaphus canadensis mitochond...	50	2e-05
dbj|AB021091.1|AB021091	Cervus nippon nippon mitochondrial ...	50	2e-05
dbj|AB021090.1|AB021090	Cervus nippon pulchellus mitochondr...	50	2e-05
dbj|AB006539.1|AB006539	Dinodon semicarinatus mitochondrial...	50	2e-05
dbj|AB006800.1|AB006800	Ovis aries mitochondrial DNA for cy...	50	2e-05
gb|L12761.1|LDHMTCYTB	Lepidochelys kempi (LK-3) mitochondri...	50	2e-05
gb|L08032.1|CPLMTCYTBA	Carcharhinus plumbeus mitochondrial ...	50	2e-05
gb|L28941.1|URRCYB	Uroderma bilobatum cytochrome b gene, 5'...	50	2e-05
gb|L28937.1|CDECYB	Chiroderma doriae cytochrome b gene, 5' end	50	2e-05
emb|AJ010056.1|CPY010056	Capra pyrenaica (individual 12) mi...	50	2e-05
emb|AJ010054.1|CPY010054	Capra pyrenaica (individual 11) mi...	50	2e-05
emb|AJ010053.1|CPY010053	Capra pyrenaica (individual 10) mi...	50	2e-05
emb|AJ010052.1|CPY010052	Capra pyrenaica (individual 9) mit...	50	2e-05
emb|AJ010051.1|CPY010051	Capra pyrenaica (individual 8) mit...	50	2e-05
emb|AJ010050.1|CPY010050	Capra pyrenaica (individual 7) mit...	50	2e-05
emb|AJ010049.1|CPY010049	Capra pyrenaica (individual 6) mit...	50	2e-05
emb|AJ010048.1|CPY010048	Capra pyrenaica (individual 5) mit...	50	2e-05
emb|AJ010047.1|CPY010047	Capra pyrenaica (individual 4) mit...	50	2e-05
emb|X95777.1|CLMCB	C.longirostris mitochondrial cytochrome ...	50	2e-05
emb|AJ009879.1|CIB9879	Capra ibex nubiana mitochondrial cyt...	50	2e-05
emb|AJ010055.1|CIB010055	Capra ibex (individual 1) ibex mit...	50	2e-05
gb|U08946.1|CAU08946	Coragyps atratus mitochondrion cytochr...	50	2e-05
gb|U08945.1|CBU08945	Cathartes burrovianus mitochondrion cy...	50	2e-05
gb|U08944.1|VGU08944	Vultur gryphus mitochondrion cytochrom...	50	2e-05
gb|U08941.1|PAU08941	Platalea alba mitochondrion cytochrome...	50	2e-05
gb|U08940.1|PRU08940	Phoenicopterus ruber mitochondrion cyt...	50	2e-05
emb|X95775.1|ACMCB	A.cristatus mitochondrial cytochrome b gene	50	2e-05
emb|X95774.1|ABMCB	A.bennettii mitochondrial cytochrome b gene	50	2e-05
emb|X95764.1|AAMCB	A.albertisi mitochondrial cytochrome b gene	50	2e-05
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gb|AF232023.1|AF232023	Tamandua tetradactyla clone 7 cytoch...	46	3e-04
gb|AF232022.1|AF232022	Tamandua tetradactyla clone 6 mitoch...	46	3e-04
gb|AF232021.1|AF232021	Tamandua tetradactyla clone 5 cytoch...	46	3e-04
gb|AF157466.1|AF157466	Lepus timidus cytochrome b (Cyb) gen...	46	3e-04
gb|AF157465.1|AF157465	Lepus granatensis cytochrome b (Cyb)...	46	3e-04
gb|AF157464.1|AF157464	Lepus corsicanus haplotype 1 cytochr...	46	3e-04
gb|AF157463.1|AF157463	Lepus corsicanus haplotype 3 cytochr...	46	3e-04
gb|AF157460.1|AF157460	Lepus europaeus cytochrome b (Cyb) g...	46	3e-04
gb|AF231664.1|AF231664	Tylosurus crocodilus crocodilus cyto...	46	3e-04
gb|AF231663.1|AF231663	Tylosurus crocodilus clone STRI-1837...	46	3e-04
gb|AF231662.1|AF231662	Tylosurus crocodilus clone HB-166 cy...	46	3e-04
gb|AF231660.1|AF231660	Tylosurus acus pacificus cytochrome ...	46	3e-04
gb|AF231659.1|AF231659	Tylosurus acus melanotus clone STRI-...	46	3e-04
gb|AF231658.1|AF231658	Tylosurus acus melanotus clone STRI-...	46	3e-04
gb|AF231657.1|AF231657	Tylosurus acus imperialis cytochrome...	46	3e-04
gb|AF231656.1|AF231656	Tylosurus acus acus cytochrome b oxi...	46	3e-04
gb|AF231644.1|AF231644	Strongylura hubbsi cytochrome b oxid...	46	3e-04
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gb|AF326270.1|AF326270	Myospalax psilurus isolate 1 cytochr...	46	3e-04
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Posted date: Mar 2, 2001 12:20 AM
Number of letters in database: 2,863,827,885
Number of sequences in database: 807,597

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Gapped Lambda	K	H
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Matrix: blastn matrix:1 -3
Gap Penalties: Existence: 5, Extension: 2
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Number of Sequences: 807597
Number of extensions: 39355
Number of successful extensions: 15066
Number of sequences better than 10.0: 5706
length of query: 25
length of database: 2,863,827,885
effective HSP length: 17
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effective search space: 22800789888
effective search space used: 22800789888
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X2: 15 (29.7 bits)
S1: 12 (24.3 bits)
S2: 16 (32.2 bits)

Table 11. BLAST analysis of primers 'mcb869' in *nr* database of NCBI. It demonstrates that the 3' end of this primer is highly conserved among a vast range of animal species. It also shows the significant homology among the primer and templates (i.e. the cytochrome b gene fragment of different animal species), confirming the universal nature of our primer.

BLASTN 2.1.2 [Nov-13-2000]

Reference:
Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 984593033-24247-14777

Query=
(26 letters)

Database: nt
807,597 sequences; 2,863,827,885 total letters

If you have any problems or questions with the results of this search please refer to the BLAST FAQs

Taxonomy reports

Distribution of 500 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments

Sequences producing significant alignments:

	Score (bits)	E Value
gb|AF189111.1|AF189111 Cryptotermes austrinus cytochrome b ...	52	6e-06
gb|U86834.1|U86834 Phyllotis wolffsohni MSB 67270 cytochrom...	52	6e-06
gb|AF123633.1|AF123633 Perissocephalus tricolor cytochrome ...	52	6e-06
gb|AF123617.1|AF123617 Pipreola arcuata cytochrome b gene, ...	52	6e-06
gb|AF127202.1|AF127202 Hylopezus fulviventris cytochrome b ...	52	6e-06
gb|AF127194.1|AF127194 Grallaria guatimalensis cytochrome b...	52	6e-06
gb|AF217828.1|AF217828 Aspidelaps scutatus cytochrome b gen...	52	6e-06
gb|AF160578.1|AF160578 Hypogeomys antimena Hant555 cytochro...	52	6e-06
gb|AF009931.2|AF009931 Archocentrus centrarchus cytochrome ...	52	6e-06
gb|AF091629.1|AF091629 Antilocapra americana cytochrome b (...	52	6e-06
gb|AF034967.1| Sigmoceros lichtensteinii cytochrome b gene,...	52	6e-06
gb|AF038290.1|AF038290 Antechinus sp. cytochrome b gene, mi...	52	6e-06
gb|U07577.1|AMU07577 Antechinus melanurus mitochondrion cyt...	52	6e-06
gb|U81343.1|CFU81343 Chelus fimbriata cytochrome b gene, mi...	52	6e-06
emb|AJ222681.1|ABCYTOB Alcelaphus buselaphus mitochondrial ...	52	6e-06
gb|M99464.1|PNZMTCYTB Planigale sp. cytochrome b gene, comp...	52	6e-06
emb|AJ225116.1|DNJ225116 Dryomys nitedula mitochondrial gen...	52	6e-06
gb|U25738.1|PRU25738 Paradisaea raggiana cytochrome b gene,...	52	6e-06
gb|U25736.1|PRU25736 Paradisaea rubra cytochrome b gene, mi...	52	6e-06
gb|U15202.1|SMU15202 Seleucidis melanoleuca mitochondrion c...	52	6e-06
gb|U15204.1|PRI5204 Paradisaea raggiana mitochondrion cytoc...	52	6e-06
emb|X56290.1|MIDDCYTB D.dama mitochondrion cytb gene for cy...	52	6e-06
emb|X56286.1|MIAACYTBA A.americana mitochondrion cytb gene ...	52	6e-06
dbj|D88639.1|D88639 Anoa depressicornis mitochondrial DNA f...	52	6e-06
dbj|D82890.1|D82890 Bubalus depressicornis mitochondrial DN...	52	6e-06
gb|AF119261.1|AF119261 Peromyscus maniculatus cytochrome b ...	46	3e-04
gb|AF123615.1|AF123615 Rupicola rupicola cytochrome b gene,...	46	3e-04
gb|AF160603.1|AF160603 Apodemus sylvaticus Asyl588 cytochro...	46	3e-04
gb|U62697.1|CCOLCYTB2 Charadrius collaris cytochrome b (cyt...	46	3e-04
gb|U62685.1|CBICCYTB2 Charadrius bicinctus cytochrome b (cy...	46	3e-04
gb|AF022071.1| Madoqua guentheri cytochrome b (cytb) gene, ...	46	3e-04
gb|AF022070.1| Madoqua kirkii cytochrome b (cytb) gene, mit...	46	3e-04
gb|U83317.1|PSU83317 Polihierax semitorquatus cytochrome b ...	46	3e-04
gb|U37293.1|CCU37293 Cepphus columba cytochrome b gene, mit...	46	3e-04
gb|U37292.1|CCU37292 Cepphus carbo cytochrome b gene, mitoc...	46	3e-04
gb|U37291.1|BMU37291 Brachyramphus marmoratus perdix cytoch...	46	3e-04
gb|AF082055.1|AF082055 Rupicola rupicola cytochrome b gene,...	46	3e-04
gb|U72770.1|JMU72770 Jabiru mycteria cytochrome b gene, mit...	46	3e-04
gb|U07578.1|DCU07578 Dasycercus cristicauda mitochondrion c...	46	3e-04
gb|AF011908.1|GOCCCYTB3 Geopsittacus occidentalis cytochrom...	46	3e-04
emb|AJ004231.1|SBAJ4231 Sula bassana mitochondrial cytb gen...	46	3e-04
emb|AJ004230.1|SBAJ4230 Sula bassana mitochondrial cytb gen...	46	3e-04
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emb|AJ004232.1|SBAJ4232 Sula bassana mitochondrial cytb gen...	46	3e-04
gb|U88865.1| Pomacentrus sp. cytochrome b (cytb) gene, mito...	46	3e-04
gb|U90001.1|MBU90001 Morus bassanus cytochrome b gene, mito...	46	3e-04
gb|U63057.1|BMU63057 Brachyramphus marmoratus perdix cytoch...	46	3e-04
dbj|AB036404.1|AB036404 Rana porosa brevipoda mitochondrial...	46	3e-04
dbj|AB036402.1|AB036402 Rana porosa brevipoda mitochondrial...	46	3e-04
dbj|AB036400.1|AB036400 Rana porosa brevipoda mitochondrial...	46	3e-04
dbj|AB036398.1|AB036398 Rana porosa porosa mitochondrial DN...	46	3e-04
gb|U19611.1|JMU19611 Jabiru mycteria cytochrome b gene, mit...	46	3e-04
emb|X92539.1|HACYTB H.ampullatus cytochrome b gene (complet...	46	3e-04
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gb|L08033.1|CPLMTCYTB8 Carcharhinus porosus mitochondrial c...	46	3e-04
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gb|U03541.2|LAU03541	Lenoxus apicalis cytochrome b gene, pa...	44	0.001
gb|AF009951.2|AF009951	Heros appendiculatus cytochrome b (c...	44	0.001
gb|AF009941.1|AF009941	Tomocichla tuba cytochrome b (cytb) ...	44	0.001
gb|AF009925.1|AF009925	Archocentrus sajica cytochrome b (cy...	44	0.001
gb|AF094633.1|AF094633	Stachyris whiteheadi cytochrome b ge...	44	0.001
gb|AF094621.1|AF094621	Eminia lepida cytochrome b gene, par...	44	0.001
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gb|AF166348.1|AF166348	Phascolarctos cinereus cytochrome b ...	44	0.001
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gb|AF022065.1|	Tragelaphus euryceros cytochrome b (cytb) ge...	44	0.001
gb|AF022059.1|	Kobus ellipsiprymnus cytochrome b (cytb) gen...	44	0.001
gb|AF022058.1|	Antilope cervicapra cytochrome b (cytb) gene...	44	0.001
gb|AF022057.1|	Tragelaphus oryx cytochrome b (cytb) gene, m...	44	0.001
gb|AF022054.1|	Antidorcas marsupialis cytochrome b (cytb) g...	44	0.001
gb|AF016637.1|AF016637	Connochaetes gnou cytochrome b (cytb...	44	0.001
gb|U69863.1|PSU69863	Python sebae cytochrome b (cytb) gene, ...	44	0.001
gb|U69844.1|LTU69844	Lichanura trivirgata cytochrome b (cyt...	44	0.001
gb|AF143193.1|AF143193	Epinephelus sp. cytochrome b (cytb) ...	44	0.001
gb|AF121222.1|AF121222	Amphiprion ocellaris isolate 8 cytoc...	44	0.001
gb|AF096625.1|AF096625	Kobus ellipsiprymnus defassa cytochr...	44	0.001
gb|AF096624.1|AF096624	Kobus ellipsiprymnus ellipsiprymnus c...	44	0.001
gb|AF081052.1|AF081052	Eulemur rubriventer cytochrome b (cy...	44	0.001
gb|AF081049.1|AF081049	Eulemur macaco macaco cytochrome b (...	44	0.001
gb|AF081048.1|AF081048	Eulemur fulvus albifrons cytochrome ...	44	0.001
gb|AF082063.1|AF082063	Elminia longicauda cytochrome b gene...	44	0.001
emb|AJ010957.1|HAAJ10957	Hippopotamus amphibius complete mi...	44	0.001
gb|U76506.1|CLU76506	Chlamydera lauterbachii cytochrome b g...	44	0.001
gb|U76504.1|CCU76504	Chlamydera cerviniventris cytochrome b...	44	0.001
gb|U76505.1|ASU76505	Amblyornis subalaris cytochrome b gene...	44	0.001
gb|U76503.1|APU76503	Archboldia papuensis cytochrome b gene...	44	0.001
gb|U76508.1|AIU76508	Amblyornis inornatus cytochrome b gene...	44	0.001
gb|AF034969.1|AF034969	Connochaetes taurinus cytochrome b g...	44	0.001
gb|AF051876.1|AF051876	Rhodeus ocellatus cytochrome b (cytb...	44	0.001
gb|AF082007.1|AF082007	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb|AF082006.1|AF082006	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb|AF082005.1|AF082005	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb|AF082004.1|AF082004	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb|AF082003.1|AF082003	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb|AF082002.1|AF082002	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb|AF082001.1|AF082001	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb|AF082000.1|AF082000	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb|AF081999.1|AF081999	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb|AF081998.1|AF081998	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb|AF081997.1|AF081997	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb|AF081996.1|AF081996	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb|AF081995.1|AF081995	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb|AF081994.1|AF081994	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb|AF081993.1|AF081993	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb|AF081992.1|AF081992	Vireo plumbeus plumbeus specimen-vou...	44	0.001

gb|AF081991.1|AF081991	Vireo plumbeus plumbeus specimen-vou...	44 0.001
gb|S73150.1|S73150	cytochrome b [Spermophilus richardsonii=...	44 0.001
gb|AF012235.1|AF012235	Cryptomys hottentotus natalensis cyt...	44 0.001
gb|U53580.1|NCU53580	Nycticebus coucang cytochrome b (cyt b...	44 0.001
gb|U53577.1|EFU53577	Eulemur fulvus rufus cytochrome b (cyt...	44 0.001
gb|U53576.1|EFU53576	Eulemur fulvus collaris cytochrome b (...	44 0.001
gb|U95512.1|ESERCYTB2	Eptesicus serotinus 3' cytochrome b (...	44 0.001
gb|U95508.1|PKUHLCYTB2	Pipistrellus kuhli 5' cytochrome b (...	44 0.001
gb|U17868.1|BTU17868	Budorcas taxicolor taxicolor cytochrom...	44 0.001
gb|U17867.1|BTU17867	Budorcas taxicolor bedfordi cytochrome...	44 0.001
gb|U17860.1|ODU17860	Ovis dalli cytochrome b gene, mitochon...	44 0.001
gb|U17859.1|OCU17859	Ovis canadensis cytochrome b gene, mit...	44 0.001
emb|AJ010556.1|ASP010556	Acomys spinosissimus mitochondrial...	44 0.001
gb|AF034736.1|AF034736	Capra falconeri cytochrome b (cytb) ...	44 0.001
gb|AF034730.1|AF034730	Ovis aries cytochrome b (cytb) gene,...	44 0.001
gb|AF034729.1|AF034729	Ovis vignei cytochrome b (cytb) gene...	44 0.001
gb|AF034728.1|	Ovis dalli dalli cytochrome b (cytb) gene, m...	44 0.001
gb|AF034727.1|	Ovis ammon darwini cytochrome b (cytb) gene,...	44 0.001
gb|AF034724.1|AF034724	Pantholops hodgsoni cytochrome b (cy...	44 0.001
gb|AF034722.1|AF034722	Addax nasomaculatus cytochrome b (cy...	44 0.001
gb|U72038.1|MMU72038	Monodon monoceros cytochrome b (cytb),...	44 0.001
gb|U72037.1|DLU72037	Delphinapterus leucas cytochrome b (cy...	44 0.001
gb|M99455.1|MUXMTCYTB	Murexia longicaudata cytochrome b gen...	44 0.001
gb|L29055.1|SHPMTDLOOP	Sheep mitochondrial cytochrome b (Cy...	44 0.001
gb|AF082047.1|AF082047	Coccyzus americanus cytochrome b gen...	44 0.001
gb|AF038286.1|AF038286	Antechinus minimus cytochrome b gene...	44 0.001
gb|AF038284.1|AF038284	Antechinus swainsonii cytochrome b g...	44 0.001
gb|AF059093.1|AF059093	Anas undulata cytochrome b gene, par...	44 0.001
gb|AF059092.1|AF059092	Anas superciliosa rogersi cytochrome...	44 0.001
gb|AF059091.1|AF059091	Anas sparsa cytochrome b gene, parti...	44 0.001
gb|AF059080.1|AF059080	Anas melleri cytochrome b gene, part...	44 0.001
gb|AF059078.1|AF059078	Anas laysanensis cytochrome b gene, ...	44 0.001
gb|AF052240.1|AF052240	Anairetes flavirostris cytochrome b ...	44 0.001
gb|AF006240.1|AF006240	Mitrospingus cassinii cytochrome b (...	44 0.001
gb|AF006227.1|AF006227	Dacnis cayana cytochrome b (cytb) ge...	44 0.001
gb|AF047447.1|AF047447	Oryx leucoryx cytochrome b gene, mit...	44 0.001
gb|U07576.1|AHU07576	Antechinus habbema mitochondrion cytoc...	44 0.001
gb|AF028180.1|AF028180	Urocyon cinereoargenteus cytochrome ...	44 0.001
gb|AF028178.1|AF028178	Pseudalopex sechurae cytochrome b (c...	44 0.001
gb|AF028170.1|AF028170	Vulpes zerda cytochrome b (cytb) gen...	44 0.001
gb|M99454.1|ASWMTSCYTB	Antechinus stuartii cytochrome b gen...	44 0.001
gb|M99453.1|ASWMTCYTB	Antechinus swainsonii cytochrome b ge...	44 0.001
gb|U23461.1|ANU23461	Antechinus naso cytochrome b gene, mit...	44 0.001
gb|U87138.1|TVU87138	Trichosurus vulpecula cytochrome b (cy...	44 0.001
gb|U07590.1|PMU07590	Planigale maculata mitochondrion cytoc...	44 0.001
emb|AJ004326.1|PTAJ4326	Phylloscopus trochilus mitochondria...	44 0.001
gb|AF020255.1|AF020255	Cyclura nubila cytochrome b (cytb) g...	44 0.001
emb|Y19184.1|LPA19184	Lama pacos complete mitochondrial genome	44 0.001
gb|U88862.1|	Amphilophus citrinellum cytochrome b (cytb) ge...	44 0.001
gb|U88859.1|	Thorichthys aureum cytochrome b (cytb) gene, m...	44 0.001
gb|U88858.1|	Thorichthys cf. aureum cytochrome b (cytb) gen...	44 0.001
gb|U88857.1|	Herichthys labridens cytochrome b (cytb) gene,...	44 0.001
gb|U88856.1|	Herichthys carpintis cytochrome b (cytb) gene,...	44 0.001
emb|Y10524.1|MIMRGEN	Macropus robustus complete mitochondri...	44 0.001
gb|U81357.1|CSU81357	Chelydra serpentina cytochrome b gene,...	44 0.001
gb|U81356.1|CLU81356	Chelodina longicollis cytochrome b gen...	44 0.001
gb|U75354.1|LUU75354	Leptomyrmex unicolor cytochrome b gene...	44 0.001
gb|U77332.1|GCU77332	Gymnorhinus cyanocephala cytochrome-b ...	44 0.001
emb|Z29573.1|OVMTGNME	Didelphis virginiana complete mitocho...	44 0.001
emb|AJ222679.1|BTCYTOB	Boselaphus tragocamelus mitochondria...	44 0.001
emb|AJ222680.1|TSCYTOB	Tragelaphus spekii mitochondrial cyt...	44 0.001
emb|AJ222685.1|ODCYTOB	Oryx dammah mitochondrial cytochrome...	44 0.001
gb|M29466.1|PMLMTCYTB	Perameles nasuta cytochrome b gene, c...	44 0.001
gb|M99457.1|THNMTCYTB	Thylacinus cynocephalus cytochrome b...	44 0.001
gb|M29460.1|DAVMTCYTB	Dasyurus hallucatus cytochrome b gene...	44 0.001
gb|U25717.1|PMU25717	Paradisaea minor cytochrome b gene, mi...	44 0.001
gb|U15201.1|PRU15201	Paradisaea rudolphi mitochondrion cyto...	44 0.001
gb|U15205.1|EAU15205	Epimachus albertisi mitochondrion cyto...	44 0.001
gb|U15200.1|DRU15200	Diphyllodes respublica mitochondrion c...	44 0.001
emb|AJ000424.1|STAJ424	Sorex tundrensis partial mitochondri...	44 0.001
emb|AJ000421.1|STAJ421	Sorex tundrensis partial mitochondri...	44 0.001

emb|AJ000438.1|SIAJ438	Sorex isodon partial mitochondrial c...	44	0.001
emb|AJ000437.1|SIAJ437	Sorex isodon partial mitochondrial c...	44	0.001
emb|AJ000428.1|SAAJ428	Sorex arcticus partial mitochondrial...	44	0.001
emb|AJ000427.1|SAAJ427	Sorex arcticus ssp. maritimensis par...	44	0.001
emb|AJ000426.1|SAAJ426	Sorex asper partial mitochondrial cy...	44	0.001
emb|AJ000425.1|SAAJ425	Sorex asper partial mitochondrial cy...	44	0.001
emb|AJ000418.1|SGAJ418	Sorex granarius partial mitochondria...	44	0.001
emb|AJ000417.1|SGAJ417	Sorex granarius partial mitochondria...	44	0.001
emb|AJ000416.1|SAAJ416	Sorex araneus partial mitochondrial ...	44	0.001
emb|AJ004793.1|HCAJ4793	Hippolais caligata ssp. caligata mi...	44	0.001
emb|AJ004792.1|HCAJ4792	Hippolais caligata ssp. rama mitoch...	44	0.001
gb|U15718.1|RSU15718	Ramphocelus sanguinolentus cytochrome ...	44	0.001
gb|L11905.1|CGYMTCYTBD	Cratogeomys gymnurus mitochondrial c...	44	0.001
gb|U34679.1|POU34679	Philander opossum cytochrome b light s...	44	0.001
gb|L11907.1|CGYMTCYTBF	Cratogeomys goldmani rubellus mitoch...	44	0.001
gb|L11906.1|CGYMTCYTBE	Cratogeomys merriami mitochondrial c...	44	0.001
gb|L11902.1|CGYMTCYTBA	Cratogeomys castanops castanops mito...	44	0.001
emb|X92524.1|SLCYTB	S.longirostris cytochrome b gene (compl...	44	0.001
gb|U46771.1|ACU46771	Anthus campestris cytochrome b gene, m...	44	0.001
dbj|AB021773.1|AB021773	Anguilla interioris mitochondrial c...	44	0.001
dbj|AB006953.1|AB006953	Carassius auratus langsdorfi mitoch...	44	0.001
emb|Z73492.1|MTPTRCYTB	P.trochilus mitochondrial cytochrome...	44	0.001
dbj|AB035239.1|AB035239	Osteoglossum ferreirai mitochondria...	44	0.001
emb|X92532.1|MMCYTB2	M.monoceros cytochrome b gene (complet...	44	0.001
emb|X74260.1|MIVOCYTB	V.olivaceus mitochondrion gene for cy...	44	0.001
emb|X56293.1|MISLCYTBB	S.longiroshis mitochondrion cytb gen...	44	0.001
emb|X56292.1|MISLCYTBA	S.longirostris mitochondrion cytb ge...	44	0.001
emb|X74256.1|MIPVCYTB	P.violaceus mitochondrion gene for cy...	44	0.001
emb|X82304.1|MIPHCYTBG	P.hispida mitochondrial cytochrome b...	44	0.001
emb|X82302.1|MIPFCYTBG	P.fasciata mitochondrial cytochrome ...	44	0.001
emb|X56284.1|MIOACYTB	O.aries mitochondrion cytb gene for c...	44	0.001
emb|X74252.1|MIMKCYTB	M.keraudrenii mitochondrion gene for ...	44	0.001
emb|X72005.1|MILWCYTB	L.weddelli mitochondrial gene for cyt...	44	0.001
emb|X74259.1|MILLCYTB	L.ludovicianus mitochondrion gene for...	44	0.001
emb|Y08814.1|MIHLCYTBG	H.liberiensis mitochondrial cytochro...	44	0.001
emb|Y08813.1|MIHACYTB	H.amphibius mitochondrial cytochrome ...	44	0.001
emb|X56287.1|MIGCCYTB	G.camelopardalis mitochondrion cytb g...	44	0.001
emb|X74253.1|MIEFCYTB	E.fastuosus mitochondrion gene for cy...	44	0.001
emb|X60941.1|MIEACB33	Epimachus albertisii mitochondrial ge...	44	0.001
emb|X74255.1|MIDMCYTB	D.magnificus mitochondrion gene for c...	44	0.001
emb|X56289.1|MICHCYTB	C.hircus mitochondrion cytb gene for ...	44	0.001
emb|V00654.1|MIBTXX	Bos taurus complete mitochondrial genome	44	0.001
emb|X60940.1|MIAMCB33	A.macgregoriae mitochondrial gene for...	44	0.001
emb|X92530.1|LACYTB	L.albirostris cytochrome b gene (comple...	44	0.001
gb|U09265.1|CAU09265	Coccyzus americanus mitochondrion cyto...	44	0.001
dbj|AB023906.1|AB023906	Petaurista leucogenys mitochondrial...	44	0.001
dbj|AB023905.1|AB023905	Petaurista leucogenys mitochondrial...	44	0.001
dbj|AB023904.1|AB023904	Petaurista leucogenys mitochondrial...	44	0.001
dbj|AB023903.1|AB023903	Petaurista leucogenys mitochondrial...	44	0.001
dbj|D88983.1|D88983	Bubalus bubalis mitochondrial DNA for c...	44	0.001
dbj|D88638.1|D88638	Bubalus bubalis mitochondrial DNA for c...	44	0.001
dbj|D88636.1|D88636	Bubalus bubalis mitochondrial DNA for c...	44	0.001
dbj|D88635.1|D88635	Bubalus bubalis mitochondrial DNA for c...	44	0.001
dbj|D88633.1|D88633	Bubalus bubalis mitochondrial DNA for c...	44	0.001
dbj|D88632.1|D88632	Bubalus bubalis mitochondrial DNA for c...	44	0.001
dbj|D88630.1|D88630	Bubalus bubalis mitochondrial DNA for c...	44	0.001
dbj|D88628.1|D88628	Bubalus bubalis mitochondrial DNA for c...	44	0.001
dbj|D88627.1|D88627	Bubalus bubalis mitochondrial DNA for c...	44	0.001
dbj|D84204.1|GOTMTCBD	Capra aegagrus mitochondrial DNA for ...	44	0.001
dbj|D84202.1|GOTMTCBB	Capra falconeri mitochondrial DNA for...	44	0.001
dbj|D82893.1|D82893	Bubalus bubalis mitochondrial DNA for c...	44	0.001
dbj|D82892.1|D82892	Bubalus bubalis mitochondrial DNA for c...	44	0.001
dbj|D82889.1|D82889	Bos javanicus mitochondrial DNA for cyt...	44	0.001
dbj|D12123.1|BBUMTCBJ	Bubalus arnee bubalis mitochondrial ...	44	0.001
dbj|D14537.1|BBUMTCBA	Bubalus bubalis mitochondrial gene fo...	44	0.001
dbj|AB004974.1|AB004974	Capra hircus mitochondrial DNA for ...	44	0.001
dbj|AB004973.1|AB004973	Capra hircus mitochondrial DNA for ...	44	0.001
dbj|AB004971.1|AB004971	Capra hircus mitochondrial DNA for ...	44	0.001
dbj|AB004952.1|AB004952	Capra aegagrus mitochondrial DNA fo...	44	0.001
dbj|D88540.1|D88540	Anoa depressicornis mitochondrial DNA f...	44	0.001
dbj|D88537.1|D88537	Bubalus bubalis mitochondrial DNA for c...	44	0.001

dbj|D88634.1|D88634	Bubalus bubalis mitochondrial DNA for c...	44	0.001
dbj|D88631.1|D88631	Bubalus bubalis mitochondrial DNA for c...	44	0.001
dbj|D88629.1|D88629	Bubalus bubalis mitochondrial DNA for c...	44	0.001
dbj|D84205.1|SHPMTCBE	Sheep mitochondrial DNA for cytochrom...	44	0.001
dbj|D84203.1|SHPMTCBC	Ovis musimon mitochondrial DNA for cy...	44	0.001
dbj|D84201.1|GOTMTCBA	Goat mitochondrial DNA for cytochrome...	44	0.001
dbj|D82894.1|D82894	Bubalus bubalis mitochondrial DNA for c...	44	0.001
dbj|D82891.1|D82891	Bubalus quarlesi mitochondrial DNA for ...	44	0.001
dbj|D34638.1|BBUMTCBB	Bubalus bubalis mitochondrial gene fo...	44	0.001
dbj|D34636.1|BOVMTCBB	Bos javanicus mitochondrial gene for ...	44	0.001
dbj|AB037602.1|AB037602	Talpa altaica mitochondrial cytb ge...	44	0.001
dbj|AB018985.1|AB018985	Cichlasoma citrinellum mitochondria...	44	0.001
dbj|AB004075.1|AB004075	Capra hircus mitochondrial DNA for ...	44	0.001
dbj|AB004073.1|AB004073	Capra hircus mitochondrial DNA for ...	44	0.001
dbj|AB004070.1|AB004070	Capra hircus mitochondrial DNA for ...	44	0.001
emb|X92531.1|DLCYTB	D.leucas cytochrome b gene (complete se...	44	0.001
gb|U07565.1|HAU07565	Hippopotamus amphibius mitochondrion c...	44	0.001
gb|U10367.1|PVU10367	Ptilonorhynchus violaceus mitochondrio...	44	0.001
gb|U10364.1|CMU10364	Chlamydera maculata mitochondrion cyto...	44	0.001
emb|Z96068.1|ASZ96068	Acomys spinosissimus DNA for mitochon...	42	0.005
gb|U76507.1|AIU76507	Amblyornis inornatus cytochrome b gene...	40	0.021
gb|AF157466.1|AF157466	Lepus timidus cytochrome b (Cyb) gen...	40	0.021
gb|AF157464.1|AF157464	Lepus corsicanus haplotype 1 cytochr...	40	0.021
gb|AF157463.1|AF157463	Lepus corsicanus haplotype 3 cytochr...	40	0.021
gb|AY016019.1|AY016018S3	Mullerornis agilis cytochrome b ge...	40	0.021
gb|AF027330.1|	Akodon olivaceus canescens museum catalog nu...	40	0.021
gb|AF027329.1|	Akodon olivaceus canescens museum catalog nu...	40	0.021
gb|AF027328.1|	Akodon olivaceus canescens museum catalog nu...	40	0.021
gb|AF027327.1|	Akodon olivaceus canescens museum catalog nu...	40	0.021
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gb|AF027323.1|	Akodon olivaceus canescens museum catalog nu...	40	0.021
gb|AF027322.1|	Akodon olivaceus beatus museum catalog numbe...	40	0.021
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gb|AF027319.1|	Akodon olivaceus beatus museum catalog numbe...	40	0.021
gb|AF027318.1|	Akodon olivaceus beatus museum catalog numbe...	40	0.021
gb|AF027317.1|	Akodon olivaceus beatus museum catalog numbe...	40	0.021
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gb|AF027313.1|	Akodon olivaceus beatus museum catalog numbe...	40	0.021
gb|AF027312.1|	Akodon olivaceus beatus museum catalog numbe...	40	0.021
gb|AF027311.1|	Akodon olivaceus brachiotis museum catalog n...	40	0.021
gb|AF027310.1|	Akodon olivaceus brachiotis museum catalog n...	40	0.021
gb|AF027309.1|	Akodon olivaceus brachiotis museum catalog n...	40	0.021
gb|AF027308.1|	Akodon olivaceus brachiotis museum catalog n...	40	0.021
gb|AF027307.1|	Akodon olivaceus brachiotis museum catalog n...	40	0.021
gb|AF266188.1|AF266188	Gillichthys mirabilis cytochrome b m...	40	0.021
gb|AF324034.1|AF324034	Phyllobates aurotaenia isolate Quebr...	40	0.021
gb|AF272639.1|AF272639	Clethrionomys gapperi specimen-vouch...	40	0.021
gb|AF272636.1|AF272636	Clethrionomys gapperi specimen-vouch...	40	0.021
gb|AF272634.1|AF272634	Clethrionomys gapperi specimen-vouch...	40	0.021
gb|AF272633.1|AF272633	Clethrionomys gapperi specimen-vouch...	40	0.021
gb|AF182711.1|AF182711	Geopelia cuneata cytochrome b gene, ...	40	0.021
gb|AF182687.1|AF182687	Columbina picui cytochrome b gene, p...	40	0.021
gb|AF155422.1|AF155422	Sigmodon ochrognathus cytochrome b (...	40	0.021
gb|AF155400.1|AF155400	Peromyscus pectoralis lacelanus cyto...	40	0.021
gb|AF155385.1|AF155385	Peromyscus attwateri isolate 1b cyto...	40	0.021
gb|AF155384.1|AF155384	Peromyscus attwateri isolate 1a cyto...	40	0.021
gb|AF155592.1|AF155592	Sigmodon ochrognathus isolate ArizAC...	40	0.021
gb|AF155591.1|AF155591	Sigmodon ochrognathus isolate McLiv7...	40	0.021
gb|AF155590.1|AF155590	Sigmodon ochrognathus isolate Duran4...	40	0.021
gb|AF155589.1|AF155589	Sigmodon ochrognathus isolate ElePt8...	40	0.021
gb|AF155588.1|AF155588	Sigmodon ochrognathus isolate Bbend4...	40	0.021
gb|AF121511.1|AF121511	Trachyphonus darnaudii cytochrome b ...	40	0.021
gb|AF264047.1|AF264047	Ursus spelaeus cytochrome b gene, co...	40	0.021
gb|AF295511.1|AF295511	Podarcis sicula cytochrome b gene, p...	40	0.021
gb|AF121706.1|AF121706	Hippocampus fisheri haplotype FK.14...	40	0.021
ref|NC_000884.1|	Cavia porcellus complete mitochondrial genome	42	0.021

gb|AF004572.1|AF004572 Arvicanthis niloticus cytochrome b (...	40	0.021
gb|AF088932.1|AF088932 Sminthopsis psammophila cytochrome b...	40	0.021
gb|U62697.1|ORUCYTB2 Oreopholus ruficollis cytochrome b (cy...	40	0.021
gb|U62681.1|CACYTB2 Charadrius australis cytochrome b (cyt ...	40	0.021
gb|U62707.1|CVERCYTB2 Charadrius veredus cytochrome b (cytb...	38	0.084
emb|AJ004315.1|HCAJ4315 Hippolais caligata mitochondrial cy...	38	0.084

Alignments

tmpseq_0	1	cctcctagtttgttagggattgatcg	26
AF189111	797	.....	772
U86834	858	.....	833
AF123633	56	.....	31
AF123617	104	.....	79
AF127202	107	.....	82
AF127194	107	.....	82
AF217828	845	.....	820
AF160578	869	.....	844
AF009931	869	.....	844
AF091629	869	.....	844
AF034967	869	.....	844
AF038290	869	.....	844
U07577	869	.....	844
U81343	791	.....	766
AJ222681	869	.....	844
M99464	869	.....	844
AJ225116	869	.....	844
U25738	872	.....	847
U25736	872	.....	847
U15202	872	.....	847
U15204	872	.....	847
X56290	869	.....	844
X56286	869	.....	844
D88639	869	.....	844
D82890	869	.....	844
AF119261	869	.....	847
AF123615	101	.....	79
AF160603	866	.....	844
U62687	179	.....	157
U62685	179	.....	157
AF022071	866	.....	844
AF022070	866	.....	844
U83317	872	.....	850
U37291	774	.....	752
U37292	774	.....	752
U37291	774	.....	752
AF082055	51	.....	29
U72770	798	.....	776
U07578	869	.....	847
AF031908	187	.....	165
AJ004231	773	.....	751
AJ004230	773	.....	751
AJ004229	773	.....	751
AJ004232	773	.....	751
U88865	850	.....	828
U90001	536	.....	514
U61057	773	.....	751
AB036404	173	.....	151
AB036402	173	.....	151
AB036400	173	.....	151
AB036398	173	.....	151
U19611	774	.....	752
X92519	869	.....	847
L08014	872	.....	850
L08011	872	.....	850
AY016012	11937	.....a.....	11912
AF074591	677	.....t.....	652
AY005212	761	.....g.....	736
AY005211	761	.....g.....	736
AF182123	797	.....c.....	772
AF182120	797	.....t.....	772

AF189118	797	.....a.....	772
AF189117	797	.....a.....	772
AF189116	797	.....g.....	772
AF112140	310	.....g.....	285
AF112139	310	.....g.....	285
AF112138	310	.....g.....	285
AF081990	872	.....t.....	847
AF081989	872	.....t.....	847
AF081988	872	.....t.....	847
AF081987	872	.....t.....	847
AF081986	872	.....t.....	847
AF081985	872	.....t.....	847
AF081984	872	.....t.....	847
AF081983	872	.....t.....	847
AF081982	872	.....t.....	847
AF081981	872	.....t.....	847
AF081980	872	.....t.....	847
AF081979	872	.....t.....	847
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AF081977	872	.....t.....	847
AF081976	872	.....t.....	847
AF081975	872	.....t.....	847
AF081974	872	.....t.....	847
AF081973	872	.....t.....	847
AF081972	872	.....t.....	847
AF081971	872	.....t.....	847
AF081970	872	.....t.....	847
AF081969	872	.....t.....	847
AF081968	872	.....t.....	847
AF081967	872	.....t.....	847
AF081966	872	.....t.....	847
AF081965	872	.....t.....	847
AF081964	872	.....t.....	847
AF081962	754	.....t.....	729
AF081961	872	.....t.....	847
AF081960	872	.....g.....	847
AF081959	872	.....t.....	847
AF112405	869	.....c.....	844
AF144317	161	.....g.....	136
AF144316	161	.....g.....	136
AF144315	161	.....g.....	136
AF144314	161	.....g.....	136
AF144313	161	.....g.....	136
AF144312	161	.....g.....	136
AF144311	161	.....g.....	136
AF144310	161	.....g.....	136
AF144309	161	.....g.....	136
NC_001567	15382	.....g.....	15357
AF212124	425	.....t.....	400
AF182706	739	.....a.....	714
AF010406	15027	.....a.....	15002
AF096452	735	.....t.....	710
AF283619	845	.....a.....	820
AF283618	845	.....a.....	820
AF283608	845	.....a.....	820
AF283602	845	.....a.....	820
AF110069	770	.....a.....	745
AF146616	95	.....g.....	70
AF271410	869	.....g.....	844
AF290132	752	.....g.....	727
NC_003504	15022	.....g.....	14997
AF161901	869	.....g.....	844
AF119261	869	.....g.....	844
AF119259	869	.....g.....	844
AF288454	91	.....a.....	66
AF161825	869	.....c.....	844
AF121642	68	.....g.....	43
AF121647	68	.....g.....	43
AF121646	104	.....g.....	77
AF121645	68	.....g.....	43
AF121644	84	.....g.....	59

[illegible]	[illegible]	.....c.....	79
AF123628	104	.....g.....	79
AF123621	85	.....g.....	60
AF123619	104	.....g.....	79
AF123618	104	.....g.....	79
AF123614	104	.....g.....	79
AF123613	101	.....g.....	76
AF127201	107	.....g.....	82
AF127192	107	.....t.....	82
AF127189	107	.....g.....	82
AF197849	872	.....g.....	847
AF197847	872	.....t.....	847
NC_000889	15040	.....g.....	15015
NC_002079	16164	.....g.....	16139
NC_001794	15052	.....a.....	15027
NC_001610	15045	.....t.....	15020
AF201612	520	.....t.....	495
AF097931	869	.....a.....	844
AF097927	869	.....g.....	844
J01394	15382	.....g.....	15357
AF168760	507	.....a.....	482
AF168759	507	.....a.....	482
AF168758	507	.....a.....	482
AF168756	507	.....a.....	482
AF182381	692	.....t.....	667
AF182380	692	.....t.....	667
U89187	872	.....a.....	847
AF193833	773	.....g.....	748
AF193822	773	.....g.....	748
AF193821	773	.....a.....	748
AF217837	845	.....t.....	820
AF217835	845	.....t.....	820
AF217834	845	.....a.....	820
AF217831	845	.....g.....	820
AF217823	845	.....a.....	820
AF217819	845	.....a.....	820
AF217815	845	.....c.....	820
AF118156	101	.....g.....	76
AF209938	418	.....a.....	393
AF209933	418	.....a.....	393
AF059104	776	.....c.....	751
AF059102	776	.....c.....	751
AF059054	776	.....c.....	751
AF192646	869	.....t.....	844
AF192645	869	.....t.....	844
AF160614	869	.....g.....	844
AF160613	869	.....g.....	844
AF160612	869	.....g.....	844
AF160611	238	.....g.....	213
AF160610	869	.....g.....	844
AF160604	869	.....g.....	844
AF160560	869	.....a.....	844
AF160559	869	.....a.....	844
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AF160553	869	.....a.....	844
AF160552	869	.....a.....	844
AF160551	869	.....a.....	844
AF160550	869	.....a.....	844
AF160549	869	.....a.....	844
AF016287	869	.....g.....	844
AF016286	869	.....g.....	844
AF016281	869	.....a.....	844
AF016281	869	.....a.....	844
AF016278	869	.....g.....	844
AF016276	869	.....a.....	844
AF016274	869	.....g.....	844
NC_001941	15027	.....a.....	15002
AF198698	869	.....a.....	844

AF108682	869	.....a.....	844
AF108673	869	.....g.....	844
AF108669	857	.....g.....	832
AF042720	869	.....a.....	844
AF042718	869	.....a.....	844
AF084082	869	.....a.....	844
AF084081	869	.....a.....	844
AF084074	869	.....a.....	844
AF090750	869	.....a.....	844
AF157939	869	.....a.....	844
AF157937	869	.....a.....	844
AF157936	869	.....a.....	844
AF157915	869	.....a.....	844
AF157914	869	.....a.....	844
AF157912	869	.....g.....	844
AF157906	869	.....g.....	844
AF157891	869	.....g.....	844
AF157882	869	.....a.....	844
AF157859	869	.....a.....	844
AF157858	869	.....a.....	844
AF157839	869	.....g.....	844
AF030497	50	.....a.....	25
U03541	869	.....g.....	844
AF009951	866	.....a.....	841
AF009941	869	.....g.....	844
AF009925	869	.....a.....	844
AF094633	737	.....g.....	712
AF094621	737	.....t.....	712
AF094618	737	.....t.....	712
AF166348	869	.....g.....	844
AF158697	869	.....a.....	844
AF158694	869	.....a.....	844
AF158693	869	.....a.....	844
AF158688	869	.....a.....	844
AF100720	869	.....a.....	844
AF091632	869	.....a.....	844
AF102815	869	.....a.....	844
AF102814	869	.....t.....	844
AF022065	869	.....a.....	844
AF022059	869	.....g.....	844
AF022058	869	.....a.....	844
AF022057	869	.....g.....	844
AF022054	869	.....a.....	844
AF016637	869	.....c.....	844
U69861	845	.....t.....	820
U69844	845	.....t.....	820
AF143193	869	.....a.....	844
AF121222	140	.....g.....	115
AF096625	869	.....g.....	844
AF096624	869	.....g.....	844
AF081052	869	.....a.....	844
AF081049	869	.....a.....	844
AF081048	869	.....g.....	844
AF082061	54	.....g.....	29
AJ010957	15040	.....g.....	15015
U76506	773	.....g.....	748
U76504	773	.....g.....	748
U76505	773	.....t.....	748
U76501	773	.....t.....	748
U76508	773	.....t.....	748
AF034969	869	.....g.....	844
AF051876	869	.....t.....	844
AF082007	872	.....t.....	847
AF082006	872	.....t.....	847
AF082005	872	.....t.....	847
AF082004	872	.....t.....	847
AF082003	872	.....t.....	847
AF082002	872	.....t.....	847
AF082001	872	.....t.....	847
AF082000	872	.....t.....	847
AF081999	872	.....t.....	847

AF081998	872	..............t..........	847
AF081997	872	..............t..........	847
AF081996	872	..............t..........	847
AF081995	872	..............t..........	847
AF081994	872	..............t..........	847
AF081993	872	..............t..........	847
AF081992	872	..............t..........	847
AF081991	872	..............t..........	847
S73150	869	....................a.....	844
AF012235	860	....................a.....	835
U51580	869	..............g..........	844
U51577	869	....................g.....	844
U51576	869	....................a.....	844
U95512	31	....................g.....	6
U95508	31	...........a.............	6
U17868	869	..............g..........	844
U17867	869	..............g..........	844
U17860	869	..............g..........	844
U17859	800	..............g..........	775
AJ010556	869	....................g.....	844
AF034736	869	..............g..........	844
AF034730	869	...........a.............	844
AF034729	869	...........a.............	844
AF034728	869	..............g..........	844
AF034727	869	...........a.............	844
AF034724	869	..............g..........	844
AF034722	869	..............g..........	844
U72038	869	..............g..........	844
U72037	869	..............g..........	844
M99455	869	...........a.............	844
L29055	260	...........a.............	235
AF082047	54	....................g.....	29
AF038286	869	..............t..........	844
AF038284	869	..............t..........	844
AF059093	776	..............t..........	751
AF059092	776	..............t..........	751
AF059091	776	..............t..........	751
AF059080	776	..............t..........	751
AF059078	776	..............t..........	751
AF052240	61	....................a.....	36
AF006240	774	..............t..........	749
AF006227	774	....................g.....	749
AF047447	41	..............g..........	16
U07576	869	..............g..........	844
AF028180	65	..............g..........	40
AF028178	69	....................g.....	44
AF028170	77	....................g.....	52
M99454	869	..................a.......	844
M99451	869	..............t..........	844
U23461	869	.........c..............	844
U87118	869	..............g..........	844
U07590	869	....................g.....	844
AJ004226	773	.....c..................	748
AF020255	819	....................g.....	794
Y19184	15022	..............g..........	14997
U88862	843	..................a.......	818
U88859	867	..............g..........	842
U88858	843	.........c..............	818
U88857	863	..............g..........	838
U88856	867	..............g..........	842
Y10524	15052	....................a.....	15027
U81357	791	..............t..........	766
U81356	791	...........a.............	766
U75354	452	..................a.......	427
U77332	872	....................g.....	847
Z29571	15045	..............t..........	15020
AJ222679	869	..............g..........	844
AJ222680	869	...........a.............	844
AJ222681	869	..............g..........	844
M92466	869	..................a.......	844
M92452	869	..............c..........	844

M99460	869	.....g.....	844
U25737	872	.....a.....	847
U15201	872	.....t.....	847
U15205	872	.....c.....	847
U15200	872	.....g.....	847
AJ000424	740	.....g.....	715
AJ000423	740	.....g.....	715
AJ000438	740	.....a.....	715
AJ000437	740	.....a.....	715
AJ000428	740	.....a.....	715
AJ000427	740	.....a.....	715
AJ000426	740	.....g.....	715
AJ000425	740	.....g.....	715
AJ000418	740	.....a.....	715
AJ000417	740	.....a.....	715
AJ000416	740	.....a.....	715
AJ004793	770	.....t.....	745
AJ004792	770	.....t.....	745
U15718	774	.....t.....	749
L11905	869	.....a.....	844
U34679	869	.....t.....	844
L11907	869	.....a.....	844
L11906	869	.....a.....	844
L11902	869	.....a.....	844
X92524	869	.....a.....	844
U46771	773	.....g.....	748
AB021773	869	.....a.....	844
AB006953	16164	.....g.....	16139
Z73492	770	.....c.....	745
AB035239	869	.....t.....	844
X92532	869	.....g.....	844
X74260	872	.....g.....	847
X56293	869	.....a.....	844
X56292	869	.....a.....	844
X74256	872	.....g.....	847
X82304	869	.....g.....	844
X82302	869	.....g.....	844
X56284	869	.....a.....	844
X74252	872	.....g.....	847
X72005	869	.....g.....	844
X74259	872	.....g.....	847
Y08814	869	.....c.....	844
Y08813	869	.....g.....	844
X56287	869	.....g.....	844
X74251	872	.....g.....	847
X60941	773	.....c.....	748
X74255	872	.....g.....	847
X56289	869	.....g.....	844
V00654	15382	.....g.....	15357
X60940	773	.....t.....	748
X92530	869	.....a.....	844
U09265	774	.....g.....	749
AB021906	842	.....a.....	817
AB021905	842	.....a.....	817
AB021904	842	.....a.....	817
AB021903	842	.....a.....	817
D88981	869	.....a.....	844
D88638	869	.....a.....	844
D88636	869	.....a.....	844
D88635	869	.....a.....	844
D88611	869	.....a.....	844
D88612	869	.....a.....	844
D88610	869	.....a.....	844
D88628	869	.....a.....	844
D88627	869	.....a.....	844
D84204	869	.....g.....	844
D84202	869	.....g.....	844
D82891	869	.....a.....	844
D82892	869	.....a.....	844
D82882	869	.....g.....	844
D12121	869	.....a.....	844

D34637	869	.....a.....	844
AB004074	869	.....g.....	844
AB004072	869	.....g.....	844
AB004071	869	.....g.....	844
AB004069	869	.....g.....	844
D88640	869	.....a.....	844
D88637	869	.....a.....	844
D88634	869	.....a.....	844
D88631	869	.....a.....	844
D88629	869	.....a.....	844
D84205	869	.....a.....	844
D84203	869	.....a.....	844
D84201	869	.....g.....	844
D82894	869	.....a.....	844
D82891	869	.....a.....	844
D34638	869	.....a.....	844
D34636	869	.....g.....	844
AB037602	869	.....a.....	844
AB018985	869	.....a.....	844
AB004075	869	.....g.....	844
AB004073	869	.....g.....	844
AB004070	869	.....g.....	844
X92531	869	.....g.....	844
U07565	869	.....g.....	844
U10367	773	.....g.....	748
U10364	773	.....g.....	748
Z96068	869	.....g.....	844
U76507	773	.....t.....	749
AF157466	791	.....	772
AF157464	793	.....	774
AF157463	793	.....	774
AY016019	93	.....	74
AF027330	869	.....	850
AF027329	869	.....	850
AF027328	869	.....	850
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AF027310	869	.....	850
AF027309	869	.....	850
AF027308	869	.....	850
AF027307	869	.....	850
AF266188	371	.....	352
AF324034	408	.....	389
AF272619	869	.....	850
AF272616	869	.....	850
AF272614	869	.....	850
AF272611	869	.....	850
AF182711	712	.....	693
AF182687	774	.....	755
AF155422	869	.....	850
AF155409	869	.....	850
AF155385	869	.....	850
AF155384	869	.....	850
AF155392	869	.....	850
AF155391	869	.....	850
AF155370	869	.....	850

AF155589	869	.....	850
AF155588	869	.....	850
AF121531	771	.....	752
AF264047	869	.....	850
AF206531	771	.....	752
AF192706	863	.....	844
NC_000884	15032	.....	15013
AF004572	869	.....	850
AF088932	869	.....	850
U62697	176	.....	157
U62681	179	.....	160
U62707	179	.....g.....n..	154
AJ004315	773	.....t.....n.....	748

Database: nt
Posted date: Mar 2, 2001 12:20 AM
Number of letters in database: 2,863,827,885
Number of sequences in database: 807,597

Lambda	K	H
1.37	0.711	1.31

Gapped

Lambda	K	H
1.37	0.711	1.31

Matrix: blastn matrix:1 -3
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 19068
Number of Sequences: 807597
Number of extensions: 19068
Number of successful extensions: 7580
Number of sequences better than 10.0: 2441
length of query: 26
length of database: 2,863,827,885
effective HSP length: 17
effective length of query: 9
effective length of database: 2,850,098,736
effective search space: 25650888624
effective search space used: 25650888624
T: 0
A: 30
X1: 6 (11.9 bits)
X2: 15 (29.7 bits)
S1: 12 (24.3 bits)
S2: 16 (32.2 bits)

Table 12. The other animals belonging to distantly related species analyzed by our primers to demonstrate its universal nature

SN.	Name of the animal
1.	Indian black buck no.1
2.	Indian black buck no 2
3	sheep
4	pig
5	dog
6	chimpanzee (chimss)
7	human (humsk)
8	Hamster
9	crocodile no1
10	crocodile no2
11	turtle no1
12	turtle no2
13	mouse
14	varanus
15	Naga-naga snake
16	Indian elephant
17	hen
18	dugong
19	lizard
20	weaver bird no1
21	weaver bird no2
22	buffalo no1
23	buffalo no 2

CLAIMS

1 Universal primers named as 'mcb 398' and 'mcb 869' capable of amplifying a fragment of cytochrome b gene of any animal species in polymerase chain reaction (PCR) and revealing the identity of the biological material of any animal of unknown origin at species and sub-species level, said primers, having the sequences:

primers name	**Sequence (5'-3')**
mcb 398	"TACCATGAGGACAAATATCATTCTG"
mcb 869	"CCTCCTAGTTTGTTAGGGATTGATCG

2. Primers as claimed in claim 1 wherein the fragment of mitochondrial cytochrome b gene is capable of significantly discriminating amongst various evolutionary lineages of different animal species.

3. Primers as claimed in claim 1 wherein the fragment of mitochondrial cytochrome b gene is flanked by the highly conserved sequences amongst a vast range of animal species.

4. Primers as claimed in claim 1 wherein the fragment on mitochondrial cytochrome b gene which is polymorphic inter-specifically, but monomorphic at intra species sources.

5. Primers as claimed in claim 1 wherein in *Antilope cervicapra* species, the sequences of the fragment mentioned under claim 1 are as follows:

Mitochondrial cytochrome b gene sequence (398-869 bp) of *Antilope cervicapra:*

"taccatgaggacaaatatctttttgaggagcaacagtcatcaccaatctcctttcagcaatcccatacatcggtacaaacctag
tagaatgaatctgaggagggttctcagtagataaagcaacccttacccgatttttcgccttccactttatcctcccatttatcattgc
agcccttaccatagtacacctactgtttctccacgaaacaggatccaacaaccccacaggaatctcatcagacgcagacaaa
attccattccacccctactacactatcaaagatatcctaggagctctactattaattttaaccctcatgcttctagtcctattctcacc
ggacctgcttggagacccagacaactatacaccagcaaacccacttaatacacccccacatatcaagcccgaatgatacttc
ctatttgcatacgcaatcctccgatcaattcctaacaaactaggagg"

6. A method for the identification of the animal from a biological sample, said method comprising the steps of:

a) isolating and amplifying the DNA from the biological sample to be tested using the primers as claimed in claim 1,

b) sequencing the amplified products,

c) blasting the sequence resolved in step (b) against mito database of National Centre for Biotechnology Information (NCBI) using BLAST program and determining the most likely family of the animal source of the biological sample.

d) blasting the sequence resolved in step (b) against non-redundant (nr) database of National Centre for Biotechnology Information (NCBI) using BLAST program and determining the most likely genus, species or more precisely the sub-species of the animal source of the biological sample,

e) identifying the most significant alignment of the sequence resolved with cytochrome b gene sequence of the animal identified in steps (c) and (d) respectively and selection of these animals as 'reference animals' for further studies,

f) isolating and amplifying and sequencing the DNA sequences from the reference animal on both strands in triplicate using the primers as claimed in claim 1,

g) aligning the sequences obtained using CLUSTRAL program and identifying the variable sites amongst the animals analyzed,

h) comparing the nucleotide sequences pair-wise to determine the variation among the animals resolved and identifying the nucleotide sequence to which the DNA sequence of the biological sample bears maximum similarity as the source animal of the biological sample.

7. A method as claimed in claim 6 wherein the universal PCR protocol works universally with the DNA template of any unknown animal origin and the universal primers mentioned under column 4.

8. A method as claimed in claim 6 wherein the Amplification reactions should be carried out in 20 µl reaction volume containing approximately 20 ηg of template DNA, 100µm each of dNTPs, 1.25 pmole of each primer, 1.5mM $MgCl_2$, 0.5 unit of Ampli*Taq* Gold (Perkin-Elmer-Cetus, USA) DNA polymerase and 1X PCR buffer (10mM Tris-HCl, pH 8.3, and 50mM KCl). The amplification profiles followed should be: an initial denaturation at 95^0C for 10 min, followed by 35 cycles each of denaturation at 95^0C for 45 s, annealing at 51^0C for 1 min, and extension at 72^0C for 2 min. The extension step at 35^{th} cycles should be held for 10 min.

9. A method as claimed in claim 6 wherein the method enables identification of species of analyzed material (i.e. the DNA isolated from confiscated animal remain of unknown origin) using the public databases such as GenBank, NCBI etc.

10. A method as claimed in claim 6 wherein the method is used for animal identification to establish the crime with the criminal beyond a reasonably doubt.

11. A method as claimed in claim 6 wherein the method is used to establish the identity of

biological materials such as skin, horns etc confiscated from animal poachers, if it is that of an endangered species.

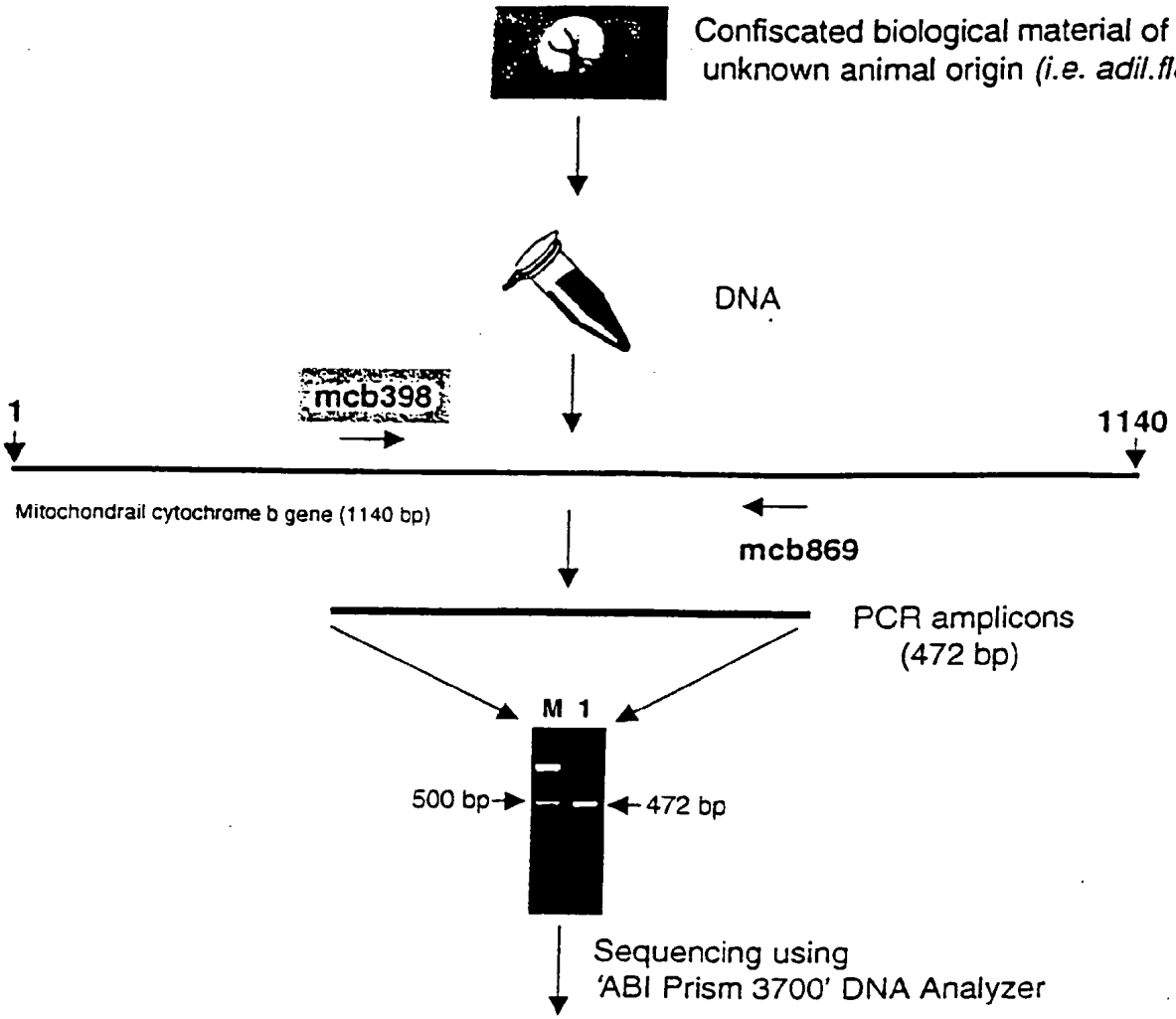
12. A method as claimed in claim 6 wherein the method is used for establishment of the identity of confiscated animal parts and products of endangered animal species for the purpose of production of molecular evidence of animal hunting and related crime in the court of law, so that the human violation of the wildlife resources could be controlled.

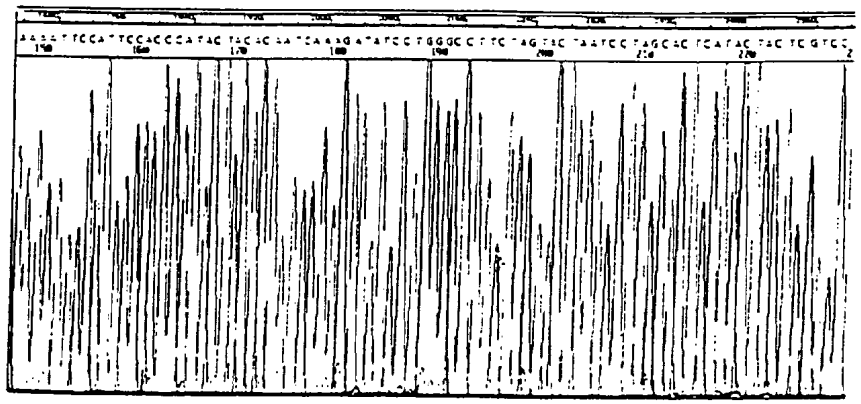
13. A method as claimed in claim 6 wherein the method is used to have an idea of the geographical location of the commitment of wildlife crime based on the cytochrome b gene haplotype of poached animal identified by the universal primer invented.

14. A method as claimed in claim 6 wherein the method is used for animal identification to detect the adulteration of animal meat in food products for the purpose of food fortification, by the food fortification agencies.

15. A method as claimed in claim 6 wherein the method is used to provide a universal technique for detection of the origin of blood or blood stains etc collected from the scene of crime related to offences such as murder, rape etc, in order to establish the origin of blood found at scene of crime when it sounds as if criminals have wontedly spread the blood of an animal at the scene of crime, to confuse the crime investigation agencies and forensic scientists with human blood.

16. A method as claimed in claim 6 wherein the method is used so that it can be converted to a (a) COMMERCIAL 'MOLECUALR KIT' and (b) 'DNA CHIPS' based applications for wildlife identification in forensics.





Revealed sequence (328 bp)

TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCTACCCTGACAC
GATTCTTTGCCTTCCACTTCATCCTTCCATTTATCATCTCAGC
TCTAGCAGCAGTCCACCTCCTATTCCTTCACGAGACAGGATCT
AACAACCCCTCAGGAATAGTATCCGACTCAGACAAAATTCCAT
TCCACCCATACTACACAATCAAAGATATCCTGGGCCTTCTAGT
ACTAATCCTAGCACTCATACTACTCGTCCTATTCTCACCAGAC
CTGTTAGGAGACCCCGATAACTACATCCCTGCCAACCCTCTAA
ATACCCCTCCCCATATCAAGCCTGAAT

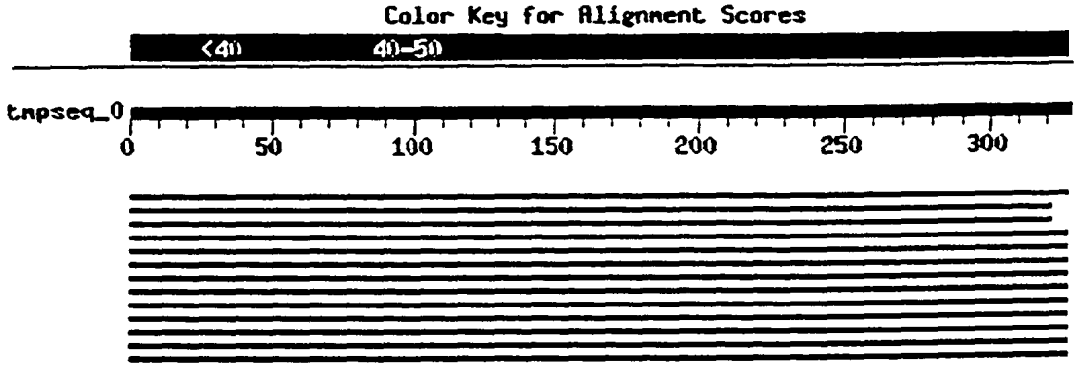
Figure 1 a

Sequence of cytochrome b gene (328 bp) revealed from biological material of unknown origin i.e. *'adil.flesh'* using primers **'mcb398'** and **'mcb869'**

Homology search in *'nr'* database using *'BLAST'*

▼

http://www.ncbi.nlm.nih.gov/BLAST/



Sequences producing significant alignments:	Score (bits)	E Value
gb|AY005809.1| *Panthera pardus* cytochrome b gene, partial c...	603	e-170
gb|AF053054.1|AF053054 *Panthera tigris sumatrae* isolate Su1...	527	e-147
gb|AF053053.1|AF053053 *Panthera tigris tigris* isolate B7 mi...	527	e-147
gb|AF053050.1|AF053050 *Panthera tigris corbetti* isolate C2 ...	476	e-132
gb|AF053049.1|AF053049 *Panthera tigris corbetti* isolate C1 ...	476	e-132

▼

Selection of reference animals based on above information and further analysis using primers **'mcb398'** and **'mcb869'**

Multiple sequence alignments using *'Autoassembler'*

▼

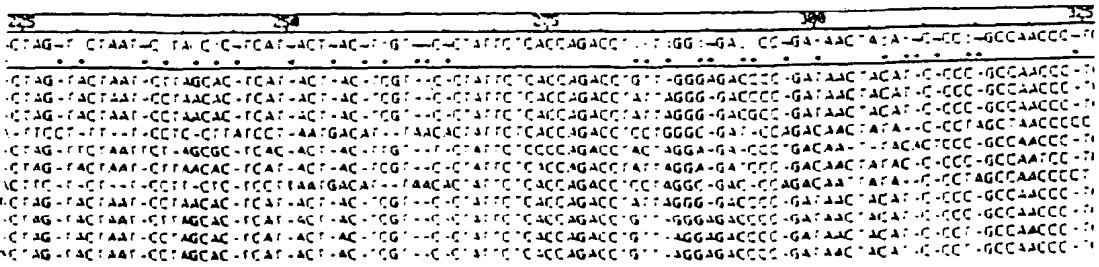


Figure 1 b

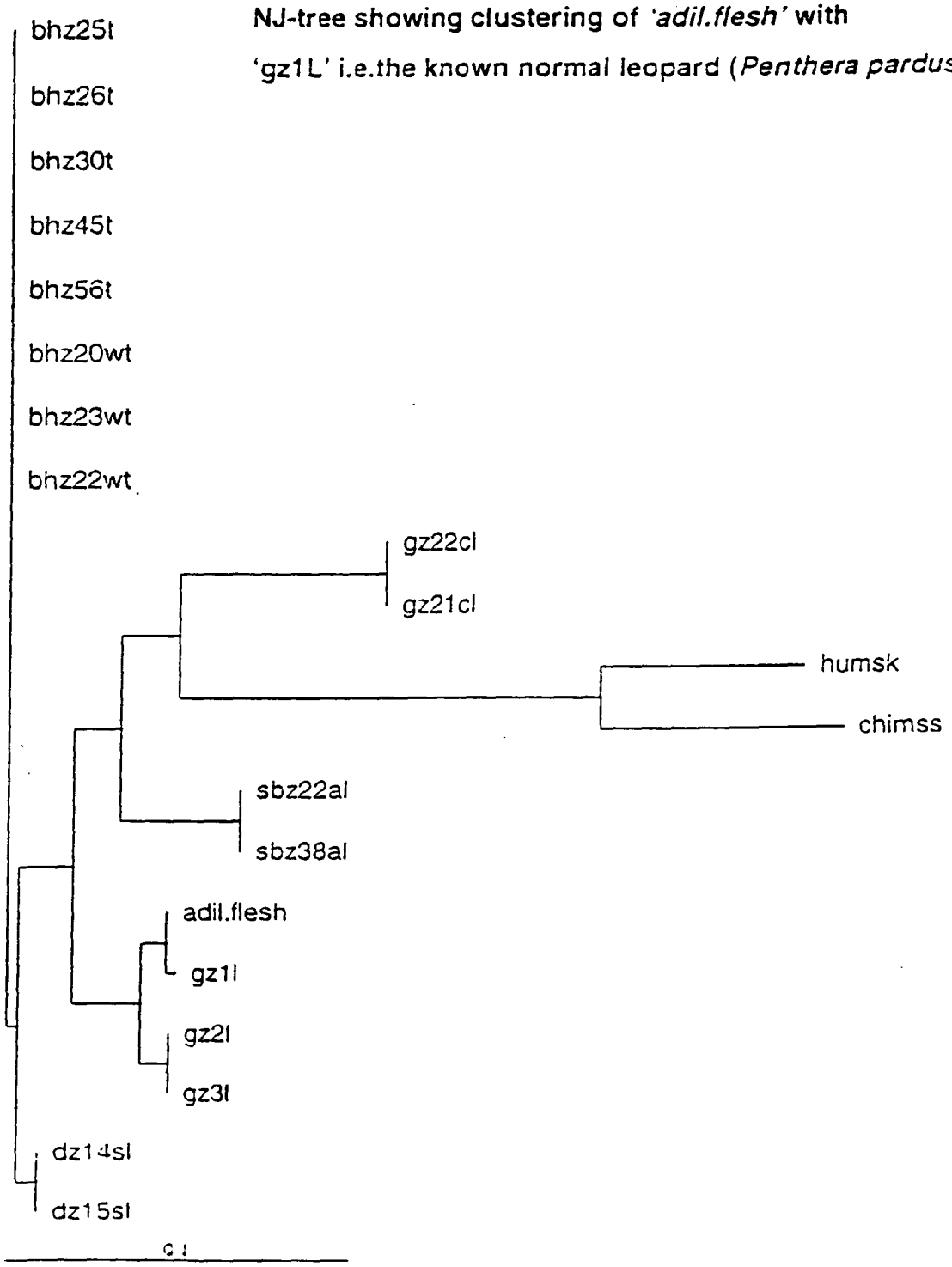

NJ-tree showing clustering of 'adil.flesh' with
'gz1L' i.e.the known normal leopard (Penthera pardus)
bhz25t
bhz26t
bhz30t
bhz45t
bhz56t
bhz20wt
bhz23wt
bhz22wt
gz22cl
gz21cl
humsk
chimss
sbz22al
sbz38al
adil.flesh
gz1l
gz2l
gz3l
dz14sl
dz15sl

Figure 1c

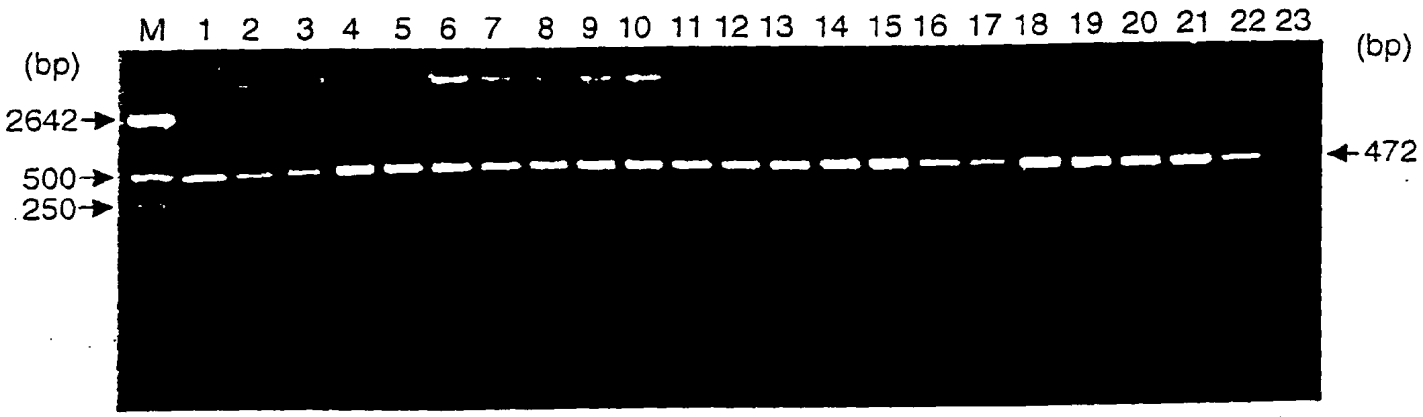

M 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23
(bp)
2642
500
250
(bp)
472

Figure 2

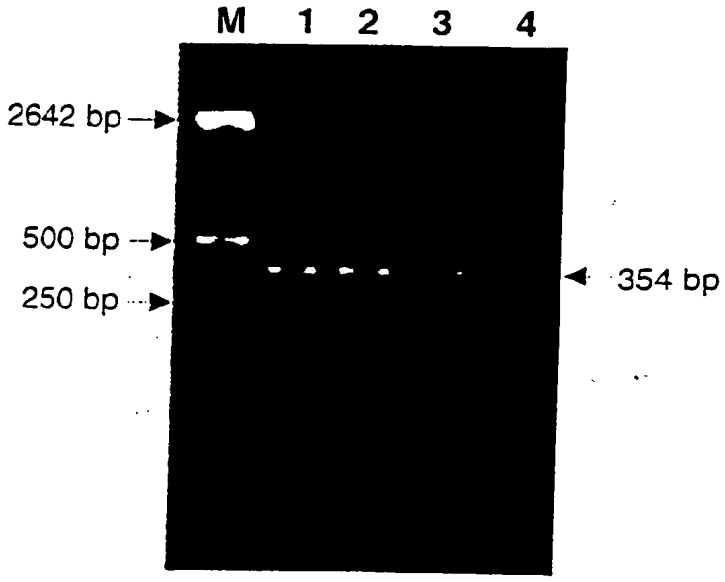


Figure 3

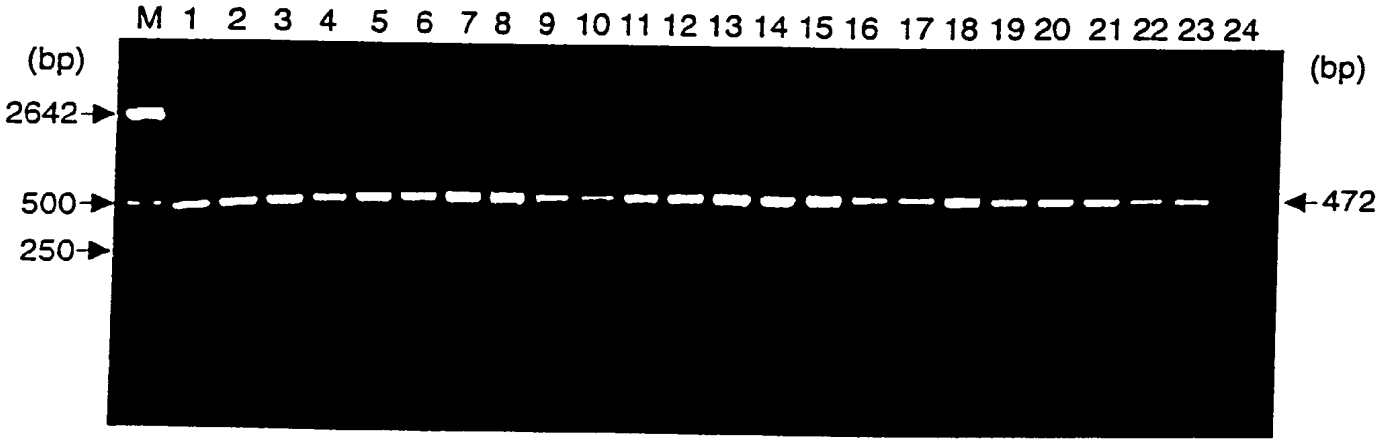

M 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24
(bp)
2642
500
250
(bp)
472

Figure 4

INTERNATIONAL SEARCH REPORT

Inte Application No
PC1/IN 01/00055

A. CLASSIFICATION OF SUBJECT MATTER
IPC 7 C12Q1/68

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 7 C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)
BIOSIS, EPO-Internal, EMBL, WPI Data, PAJ, MEDLINE, EMBASE

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
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Y	WO 92 05277 A (DAVIDSON WILLIAM SCOTT ;BARTLETT SYLVIA ERNESTINE (CA)) 2 April 1992 (1992-04-02) the whole document ---	1-16

-/--

[X] Further documents are listed in the continuation of box C.

[X] Patent family members are listed in annex.

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"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
28 February 2002	12/03/2002

Name and mailing address of the ISA	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax: (+31-70) 340-3016	Hagenmaier, S

Form PCT/ISA/210 (second sheet) (July 1992)

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication,where appropriate, of the relevant passages	Relevant to claim No.
Y	IRWIN D M ET AL: "EVOLUTION OF THE CYTOCHROME BETA GENE OF MAMMALS" JOURNAL OF MOLECULAR EVOLUTION, SPRINGER VERLAG, NEW YORK, NY, US, vol. 2, no. 3, June 1995 (1995-06), pages 128-144, XP000892117 ISSN: 0022-2844 the whole document	1-16
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Y	MATTHEE CONRAD A ET AL: "Cytochrome b phylogeny of the family Bovidae: Resolution within the Alcelaphini, Antilopini, Neotragini, and Tragelaphini." MOLECULAR PHYLOGENETICS AND EVOLUTION, vol. 12, no. 1, June 1999 (1999-06), pages 31-46, XP001053239 ISSN: 1055-7903 the whole document	1-16
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A	THOMPSON JULIE D ET AL: "A comprehensive comparison of multiple sequence alignment programs." NUCLEIC ACIDS RESEARCH, vol. 27, no. 13, 1 July 1999 (1999-07-01), pages 2682-2690, XP002191669 ISSN: 0305-1048 the whole document	

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Int l Application No
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		WO 9743618 A2	20-11-1997